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App. No.: 09/466,778
Docket No.: PF487
Inventor: Hastings et al.
Title: Novel Hyaluronan-binding Protein Encoding Genes
Replacement Sheet

FIGURE 1A

```
                .         .         .         .         .         .
  1   CTGCGACCGGTCTGCCACTTGCCAGGTGACCGCTGATGGGAAGACCAGCTGTGTGTGCAG    60

                .         .         .         .         .         .
 61   GGAAAGCGAGGTGGGGGATGGGCGTGCCTGCTACGGACACCTGCTCCACGAGGTGCAGAA   120

                .         .         .         .         .         .
121   GGCCACGCAGACAGGCCGGGTGTTCCTGCAGCTGAGGGTCGCCGTGGCCATGATGGACCA   180
  1                                                   M  M  D  Q     4

                .         .         .         .         .         .
181   GGGCTGCCGGGAAATCCTTACCACAGCGGGCCCTTTCACCGTGCTGGTGCCATCCGTCTC   240
  5    G  C  R  E  I  L  T  T  A  G  P  F  T  V  L  V  P  S  V  S    24

                .         .         .         .         .         .
241   CTCCTTCTCCTCCAGGACCATGAATGCATCCCTTGCCCAGCAGCTCTGTAGACAGCACAT   300
 25    S  F  S  S  R  T  M  N  A  S  L  A  Q  Q  L  C  R  Q  H  I    44

                .         .         .         .         .         .
301   CATCGCAGGGCAGCACATCCTGGAGGACACAAGGACCCAACAAACACGAAGGTGGTGGAC   360
 45    I  A  G  Q  H  I  L  E  D  T  R  T  Q  Q  T  R  R  W  W  T    64

                .         .         .         .         .         .
361   GCTGGCCGGGCAGGAGATCACCGTCACCTTTAACCAATTCACGAAATACTCCTACAAGTA   420
 65    L  A  G  Q  E  I  T  V  T  F  N  Q  F  T  K  Y  S  Y  K  Y    84
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FIGURE 1B

```
421  CAAAGACCAGCCCCAGCAGACGTTCAACATCTACAAGGCCAACAACATAGCAGCTAATGG  480
 85   K  D  Q  P  Q  Q  T  F  N  I  Y  K  A  N  N  I  A  A  N  G   104

481  CGTCTTCCACGTGGTCACTGGCCTGCGGTGGCAGGCCCCCTCTGGGACCCCTGGGGATCC  540
105   V  F  H  V  V  T  G  L  R  W  Q  A  P  S  G  T  P  G  D  P   124

541  CAAGAGAACTATCGGACAGATCCTCGCCTCTACCGAGGCCTTCAGCCGCTTTGAAACCAT  600
125   K  R  T  I  G  Q  I  L  A  S  T  E  A  F  S  R  F  E  T  I   144

601  CCTGGAGAACTGTGGGCTGCCCTCCATCCTGGACGGACCTGGGCCCTTCACAGTCTTTGC  660
145   L  E  N  C  G  L  P  S  I  L  D  G  P  G  P  F  T  V  F  A   164

661  CCCAAGCAATGAGGCTGTGGACAGCTTGCGTGACGGCCGCCTGATCTACCTCTTCACAGC  720
165   P  S  N  E  A  V  D  S  L  R  D  G  R  L  I  Y  L  F  T  A   184

721  GGGTCTCTCTAAACTGCAGGAGTTGGTGCGGTACCACATCTACAACCACGGCCAGCTGAC  780
185   G  L  S  K  L  Q  E  L  V  R  Y  H  I  Y  N  H  G  Q  L  T   204

781  CGTTGAGAAGCTCATCTCCAAGGGTCGGATCCTCACCATGGCGAACCAGGTCCTGGCTGT  840
205   V  E  K  L  I  S  K  G  R  I  L  T  M  A  N  Q  V  L  A  V   224
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FIGURE 1C

```
841   GAACATTTCTGAGGAGGGGCGCATCCTGCTGGGACCCGAGGGGGTCCCGCTGCAGAGGGT   900
225    N  I  S  E  E  G  R  I  L  L  G  P  E  G  V  P  L  Q  R  V    244

901   AGACGTGATGGCCGCCAATGGCGTGATCCACATGCTGGACGGCATCCTGCTGCCCCCGAC   960
245    D  V  M  A  A  N  G  V  I  H  M  L  D  G  I  L  L  P  P  T    264

961   CATCCTGCCCATCCTGCCCAAGCACTGCAGCGAGGAGCAGCACAAGATTGTGGCGGGCTC   1020
265    I  L  P  I  L  P  K  H  C  S  E  E  Q  H  K  I  V  A  G  S    284

1021  CTGTGTGGACTGCCAAGCCCTGAACACCAGCACGTGTCCCCCCAACAGTGTGAAGCTGGA   1080
285    C  V  D  C  Q  A  L  N  T  S  T  C  P  P  N  S  V  K  L  D    304

1081  CATCTTCCCCAAGGAGTGTGTCTACATCCATGACCCAACGGGGCTCAATGTGCTAAAGAA   1140
305    I  F  P  K  E  C  V  Y  I  H  D  P  T  G  L  N  V  L  K  K    324

1141  GGGCTGTGCCAGCTACTGCAACCAAACCATCATGGAACAAGGCTGCTGCAAAGGTTTTTT   1200
325    G  C  A  S  Y  C  N  Q  T  I  M  E  Q  G  C  C  K  G  F  F    344

1201  CGGGCCTGACTGCACGCAGTGTCCTGGGGGCTTCTCCAACCCCTGCTATGGCAAAGGCAA   1260
345    G  P  D  C  T  Q  C  P  G  G  F  S  N  P  C  Y  G  K  G  N    364
```

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FIGURE 1D

```
                                                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1261  TTGCAGTGATGGGATCCAGGGCAATGGGGCCTGCCTCTGCTTCCCAGACTACAAGGGCAT   1320
 365   C  S  D  G  I  Q  G  N  G  A  C  L  C  F  P  D  Y  K  G  I    384

      ~~~~~~
1321  CGCCTGCCACATCTGCTCGAACCCAAACAAGCATGGAGAGCAATGCCAGGAAGACTGCGG   1380
 385   A  C  H  I  C  S  N  P  N  K  H  G  E  Q  C  Q  E  D  C  G    404

1381  CTGTGTCCATGGTCTCTGCGACAACCGCCCAGGCAGTGGGGGGGTGTGCCAGCAGGGCAC   1440
 405   C  V  H  G  L  C  D  N  R  P  G  S  G  G  V  C  Q  Q  G  T    424

1441  GTGTGCCCCTGGCTTCAGTGGCCGGTTCTGCAACGAGTCCATGGGGGACTGTGGGCCCAC   1500
 425   C  A  P  G  F  S  G  R  F  C  N  E  S  M  G  D  C  G  P  T    444

1501  AGGGCTGGCCCAGCACTGCCACCTGCATGCCCGCTGTGTTAGCCAGGAGGGTGTTGCCAG   1560
 445   G  L  A  Q  H  C  H  L  H  A  R  C  V  S  Q  E  G  V  A  R    464

1561  ATGTCGCTGTCTTGATGGCTTTGAGGGTGATGGCTTCTCCTGCACACCTAGCAACCCCTG   1620
 465   C  R  C  L  D  G  F  E  G  D  G  F  S  C  T  P  S  N  P  C    484

1621  CTCCCACCCGGACCGTGGAGGCTGCTCAGAGAATGCTGAGTGTGTCCCTGGGTCCCTGGG   1680
 485   S  H  P  D  R  G  G  C  S  E  N  A  E  C  V  P  G  S  L  G    504
```

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FIGURE 1E

```
1681  CACCCACCACTGCACATGCCACAAAGGCTGGAGTGGGGATGGCCGCGTCTGTGTGGCTAT  1740
 505   T  H  H  C  T  C  H  K  G  W  S  G  D  G  R  V  C  V  A  I   524

1741  TGACGAGTGTGAGCTGGACGTGAGAGGTGGCTGCCACACCGATGCCCTCTGCAGCTATGT  1800
 525   D  E  C  E  L  D  V  R  G  G  C  H  T  D  A  L  C  S  Y  V   544

1801  GGGCCCCGGGCAGAGCCGATGCACCTGCAAGCTGGGCTTTGCCGGGGATGGCTACCAGTG  1860
 545   G  P  G  Q  S  R  C  T  C  K  L  G  F  A  G  D  G  Y  Q  C   564

1861  CAGCCCCATCGACCCCTGCCGGGCAGGCAATGGCGGCTGCCACGGCCTGGAGCTGGAGGC  1920
 565   S  P  I  D  P  C  R  A  G  N  G  G  C  H  G  L  E  L  E  A   584

1921  AAATGCCCACTTCTCCATCTTCTACCAATGGCTTAAGAGTGCCGGCATCACGCTTCCTGC  1980
 585   N  A  H  F  S  I  F  Y  Q  W  L  K  S  A  G  I  T  L  P  A   604

1981  CGACCGCCGAGTCACAGCCCTGGTGCCCTCCGAGGCTGCAGTCCGTCAGCTGAGCCCCGA  2040
 605   D  R  R  V  T  A  L  V  P  S  E  A  A  V  R  Q  L  S  P  E   624

2041  GGACCGAGCTTTCTGGCTGCAGCCAAGGACGCTGCCGAACCTGGTCAGGGCCCATTTTCT  2100
 625   D  R  A  F  W  L  Q  P  R  T  L  P  N  L  V  R  A  H  F  L   644
```

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FIGURE 1F

```
2101  CCAGGGTGCCCTCTTCGAGGAGGAGCTGGCCCGGCTGGGTGGGCAGGAAGTGGCCACCCT  2160
 645    Q   G   A   L   F   E   E   E   L   A   R   L   G   G   Q   E   V   A   T   L    664

2161  GAACCCCACCACACGCTGGGAGATTCGCAACATTAGTGGGAGGGTCTGGGTGCAGAATGC  2220
 665    N   P   T   T   R   W   E   I   R   N   I   S   G   R   V   W   V   Q   N   A    684

2221  CAGCGTGGATGTGGCTGACCTCCTTGCCACCAACGGTGTCCTACACATCCTCAGCCAGGT  2280
 685    S   V   D   V   A   D   L   L   A   T   N   G   V   L   H   I   L   S   Q   V    704

2281  CTTACTGCCCCCCCGAGGGGATGTGCCCGGTGGGCAGGGGTTGCTGCAGCAGCTGGACTT  2340
 705    L   L   P   P   R   G   D   V   P   G   G   Q   G   L   L   Q   Q   L   D   L    724

2341  GGTGCCTGCCTTCAGCCTCTTCCGGGAATTGCTGCAGCACCATGGGTTGGTGCCCCAGAT  2400
 725    V   P   A   F   S   L   F   R   E   L   L   Q   H   H   G   L   V   P   Q   I    744

2401  TGAGGCTGCCACTGCCTACACCATCTTTGTGCCCACCAACCGCTCCCTGGAGGCCCAGGG  2460
 745    E   A   A   T   A   Y   T   I   F   V   P   T   N   R   S   L   E   A   Q   G    764

2461  CAACAGCAGTCACCTGGACGCAGACACAGTGCGGCACCATGTGGTCCTGGGGGAGGCCCT  2520
 765    N   S   S   H   L   D   A   D   T   V   R   H   H   V   V   L   G   E   A   L    784
```

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FIGURE 1G

```
2521  CTCCATGGAAACCCTGCGGAAGGGTGGACACCGCAACTCCCTCCTGGGCCCTGCCCACTG  2580
 785   S  M  E  T  L  R  K  G  G  H  R  N  S  L  L  G  P  A  H  W   804

2581  GATCGTCTTCTACAACCACAGTGGCCAGCCTGAGGTGAACCATGTGCCACTGGAAGGCCC  2640
 805   I  V  F  Y  N  H  S  G  Q  P  E  V  N  H  V  P  L  E  G  P   824

2641  CATGCTGGAGGCCCCTGGCCGCTCGCTGATTGGTCTGTCGGGGGTCCTGACGGTGGGCTC  2700
 825   M  L  E  A  P  G  R  S  L  I  G  L  S  G  V  L  T  V  G  S   844

2701  AAGTCGCTGCCTGCATAGCCACGCTGAGGCCCTGCGGGAGAAATGTGTAAACTGCACCAG  2760
 845   S  R  C  L  H  S  H  A  E  A  L  R  E  K  C  V  N  C  T  R   864

2761  GAGATTCCGCTGCACTCAGGGCTTCCAGCTGCAGGACACACCCAGGAAGAGCTGTGTCTA  2820
 865   R  F  R  C  T  Q  G  F  Q  L  Q  D  T  P  R  K  S  C  V  Y   884

2821  CCGATCTGGCTTCTCCTTCTCCCGGGGCTGCTCTTACACATGTGCCAAGAAGATCCAGGT  2880
 885   R  S  G  F  S  F  S  R  G  C  S  Y  T  C  A  K  K  I  Q  V   904

2881  GCCGGACTGCTGCCCTGGTTTCTTTGGCACGCTGTGTGAGCCATGCCCAGGGGGTCTAGG  2940
 905   P  D  C  C  P  G  F  F  G  T  L  C  E  P  C  P  G  G  L  G   924
```

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FIGURE 1H

```
                                                                  ~~~~~~
2941  GGGGGTGTGCTCAGGCCATGGGCAGTGCCAGGACAGGTTCCTGGGCAGCGGGGAGTGCCA   3000
 925   G  V  C  S  G  H  G  Q  C  Q  D  R  F  L  G  S  G  E  C  H    944

      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3001  CTGCCACGAGGGCTTCCATGGAACGGCCTGTGAGGTGTGTGAGCTGGGCCGCTACGGGCC   3060
 945   C  H  E  G  F  H  G  T  A  C  E  V  C  E  L  G  R  Y  G  P    964

3061  CAACTGCACCGGAGTGTGTGACTGTGCCCATGGGCTGTGCCAGGAGGGGCTGCAAGGGGA   3120
 965   N  C  T  G  V  C  D  C  A  H  G  L  C  Q  E  G  L  Q  G  D    984

         ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3121  CGGAAGCTGTGTCTGTAACGTGGGCTGGCAGGGCCTCCGCTGTGACCAGAAAATCACCAG   3180
 985   G  S  C  V  C  N  V  G  W  Q  G  L  R  C  D  Q  K  I  T  S   1004

3181  CCCTCAGTGCCCTAGGAAGTGCGACCCCAATGCCAACTGCGTGCAGGACTCGGCCGGAGC   3240
1005   P  Q  C  P  R  K  C  D  P  N  A  N  C  V  Q  D  S  A  G  A   1024

3241  CTCCACCTGCGCCTGTGCTGCGGGATACTCCGGCAATGGCATCTTCTGTTCAGAGGTGGA   3300
1025   S  T  C  A  C  A  A  G  Y  S  G  N  G  I  F  C  S  E  V  D   1044

3301  CCCCTGCGCCCACGGCCATGGGGGCTGCTCCCCTCATGCCAACTGTACCAAGGTGGCACC   3360
1045   P  C  A  H  G  H  G  G  C  S  P  H  A  N  C  T  K  V  A  P   1064
```

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FIGURE 1I

```
3361  TGGGCAGCGGACATGCACCTGCCAGGATGGCTACATGGGCGACGGGGAGCTGTGCCAGGA  3420
1065   G  Q  R  T  C  T  C  Q  D  G  Y  M  G  D  G  E  L  C  Q  E   1084

3421  AATTAACAGCTGTCTCATCCACCACGGGGGCTGCCACATTCACGCCGAGTGCATCCCCAC  3480
1085   I  N  S  C  L  I  H  H  G  G  C  H  I  H  A  E  C  I  P  T   1104

3481  TGGCCCCCAGCAGGTCTCCTGCAGCTGCCGTGAGGGTTACAGCGGGGATGGCATCCGGAC  3540
1105   G  P  Q  Q  V  S  C  S  C  R  E  G  Y  S  G  D  G  I  R  T   1124

3541  CTGCGAGCTCCTGGACCCCTGCTCTAAGAACAATGGAGGATGCAGCCCATATGCCACCTG  3600
1125   C  E  L  L  D  P  C  S  K  N  N  G  G  C  S  P  Y  A  T  C   1144

3601  CAAAAGCACAGGGGATGGCCAGAGGACATGTACCTGCGACACAGCCCACACCGTGGGGGA  3660
1145   K  S  T  G  D  G  Q  R  T  C  T  C  D  T  A  H  T  V  G  D   1164

3661  CGGCCTCACCTGCCGTGCCCGAGTCGGCCTGGAGCTCCTGAGGGATAAGCATGCCTCATT  3720
1165   G  L  T  C  R  A  R  V  G  L  E  L  L  R  D  K  H  A  S  F   1184

3721  CTTCAGCCTCCGCCTCCTGGAATATAAGGAGCTCAAGGGCGATGGGCCTTTCACCATCTT  3780
1185   F  S  L  R  L  L  E  Y  K  E  L  K  G  D  G  P  F  T  I  F   1204
```

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FIGURE 1J

```
3781  CGTGCCGCACGCAGATCTAATGAGCAACCTGTCGCAGGATGAGCTGGCCCGGATTCGTGC  3840
1205   V  P  H  A  D  L  M  S  N  L  S  Q  D  E  L  A  R  I  R  A   1224

3841  GCATCGCCAGCTGGTGTTTCGCTACCACGTGGTTGGCTGTCGGCGGCTGCGGAGCGAGGA  3900
1225   H  R  Q  L  V  F  R  Y  H  V  V  G  C  R  R  L  R  S  E  D   1244

3901  CCTGCTGGAGCAGGGGTACGCCACGGCCCTCTCAGGGCACCCACTGCGCTTCAGCGAGAG  3960
1245   L  L  E  Q  G  Y  A  T  A  L  S  G  H  P  L  R  F  S  E  R   1264

3961  GGAGGGCAGCATATACCTCAATGACTTCGCGCGCGTGGTGAGCAGCGACCATGAGGCCGT  4020
1265   E  G  S  I  Y  L  N  D  F  A  R  V  V  S  S  D  H  E  A  V   1284

4021  GAACGGCATCCTGCACTTCATTGACCGTGTCCTGCTGCCCCCCGAGGCGCTGCACTGGGA  4080
1285   N  G  I  L  H  F  I  D  R  V  L  L  P  P  E  A  L  H  W  E   1304

4081  GCCTGATGATGCTCCCATCCCGAGGAGAAATGTCACCGCCGCCGCCCAGGGCTTCGGTTA  4140
1305   P  D  D  A  P  I  P  R  R  N  V  T  A  A  A  Q  G  F  G  Y   1324

4141  CAAGATCTTCAGCGGCCTCCTGAAGGTGGCCGGCCTCCTGCCCCTGCTTCGAGAGGCATC  4200
1325   K  I  F  S  G  L  L  K  V  A  G  L  L  P  L  L  R  E  A  S   1344
```

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FIGURE 1K

```
4201  CCATAGGCCCTTCACAATGCTGTGGCCCACAGACGCCGCCTTTCGAGCTCTGCCTCCGGA  4260
1345   H  R  P  F  T  M  L  W  P  T  D  A  A  F  R  A  L  P  P  D   1364

4261  TCGCCAGGCCTGGCTGTACCATGAGGACCACCGTGACAAGCTAGCAGCCATTCTGCGGGG  4320
1365   R  Q  A  W  L  Y  H  E  D  H  R  D  K  L  A  A  I  L  R  G   1384

4321  CCACATGATTCGCAATGTCGAGGCCTTGGCATCTGACCTGCCCAACCTGGGCCCACTTCG  4380
1385   H  M  I  R  N  V  E  A  L  A  S  D  L  P  N  L  G  P  L  R   1404

4381  AACCATGCATGGGACCCCCATCTCTTTCTCCTGCAGCCGAACGCGGCCCGGTGAGCTCAT  4440
1405   T  M  H  G  T  P  I  S  F  S  C  S  R  T  R  P  G  E  L  M   1424

4441  GGTGGGTGAGGATGATGCTCGCATTGTGCAGCGGCACTTGCCCTTTGAGGGTGGCCTGGC  4500
1425   V  G  E  D  D  A  R  I  V  Q  R  H  L  P  F  E  G  G  L  A   1444

4501  CTATGGCATCGACCAGCTGCTGGAGCCACCTGGCCTTGGTGCTCGCTGTGACCACTTTGA  4560
1445   Y  G  I  D  Q  L  L  E  P  P  G  L  G  A  R  C  D  H  F  E   1464

4561  GACCCGGCCCCTGCGACTGAACACCTGCAGCATCTGTGGGCTGGAGCCACCCTGTCCTGA  4620
1465   T  R  P  L  R  L  N  T  C  S  I  C  G  L  E  P  P  C  P  E   1484
```

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FIGURE 1L

```
4621  GGGGTCACAGGAGCAGGGCAGCCCTGAGGCCTGCTGGCGCTTCTACCCGAAGTTCTGGAC   4680
1485   G  S  Q  E  Q  G  S  P  E  A  C  W  R  F  Y  P  K  F  W  T    1504

4681  GTCCCCTCCGCTGCACTCTTTGGGATTACGCAGCGTCTGGGTCCACCCCAGCCTTTGGGG   4740
1505   S  P  P  L  H  S  L  G  L  R  S  V  W  V  H  P  S  L  W  G    1524

4741  TAGGCCCCAAGGCCTGGGCAGGGGCTGCCACCGCAATTGTGTCACCACCACCTGGAAGCC   4800
1525   R  P  Q  G  L  G  R  G  C  H  R  N  C  V  T  T  T  W  K  P    1544

4801  CAGCTGCTGCCCTGGTCACTATGGCAGTGAGTGCCAAGCTTGCCCTGGCGGCCCCAGCAG   4860
1545   S  C  C  P  G  H  Y  G  S  E  C  Q  A  C  P  G  G  P  S  S    1564

                                                    ~~~~~~~~~~
4861  CCCTTGTAGTGACCGTGGCGTGTGCATGGACGGCATGAGTGGCAGTGGGCAGTGTCTGTG   4920
1565   P  C  S  D  R  G  V  C  M  D  G  M  S  G  S  G  Q  C  L  C    1584

      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
4921  CCGTTCAGGTTTTGCTGGGACAGCCTGTGAACTCTGTGCTCCTGGTGCCTTTGGGCCCCA   4980
1585   R  S  G  F  A  G  T  A  C  E  L  C  A  P  G  A  F  G  P  H    1604

4981  TTGTCAAGCCTGCCGCTGCACTGTGCATGGCCGCTGTGATGAGGGCCTTGGGGGCTCTGG   5040
1605   C  Q  A  C  R  C  T  V  H  G  R  C  D  E  G  L  G  G  S  G    1624
```

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FIGURE 1M

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FIGURE 1N

```
5461  GGAACCACCTGTGGACCGCTGCTTGGGCCAGCCACCGCCCTGCCACTCAGATGCCATGTG  5520
1765   E  P  P  V  D  R  C  L  G  Q  P  P  P  C  H  S  D  A  M  C   1784

5521  CACTGACCTGCACTTCCAGGAGAAACGGGCTGGCGTTTTCCACCTCCAGGCCACCAGCGG  5580
1785   T  D  L  H  F  Q  E  K  R  A  G  V  F  H  L  Q  A  T  S  G   1804

                                  **************************
5581  CCCTTATGGTCTGAACTTTTCGGAGGCTGAGGCGGCATGCGAAGCACAGGGAGCCGTCCT  5640
1805   P  Y  G  L  N  F  S  E  A  E  A  A  C  E  A  Q  G  A  V  L   1824

      ************************************************************
5641  TGCTTCATTCCCTCAGCTCTCTGCTGCCCAGCAGCTGGGCTTCCACCTGTGCCTCATGGG  5700
1825   A  S  F  P  Q  L  S  A  A  Q  Q  L  G  F  H  L  C  L  M  G   1844

      ******************************************************
5701  CTGGCTGGCCAATGGCTCCACTGCCCACCCTGTGGTTTTCCCTGTGGCGGACTGTGGCAA  5760
1845   W  L  A  N  G  S  T  A  H  P  V  V  F  P  V  A  D  C  G  N   1864

5761  TGGTCGGGTGGGCATAGTCAGCCTGGGTGCCCGCAAGAACCTCTCAGAACGCTGGGATGC  5820
1865   G  R  V  G  I  V  S  L  G  A  R  K  N  L  S  E  R  W  D  A   1884

5821  CTACTGCTTCCGTGTGCAAGATGTGGCCTGCCGATGCCGAAATGGCTTCGTGGGTGACGG  5880
1885   Y  C  F  R  V  Q  D  V  A  C  R  C  R  N  G  F  V  G  D  G   1904
```

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FIGURE 10

```
5881  GATCAGCACGTGCAATGGGAAGCTGCTGGATGTGCTGGCTGCCACTGCCAACTTCTCCAC  5940
1905   I  S  T  C  N  G  K  L  L  D  V  L  A  A  T  A  N  F  S  T   1924

5941  CTTCTATGGGATGCTATTGGGCTATGCCAATGCCACCCAGCGGGGTCTCGACTTCCTGGA  6000
1925   F  Y  G  M  L  L  G  Y  A  N  A  T  Q  R  G  L  D  F  L  D   1944

6001  CTTCCTGGATGATGAGCTCACGTATAAGACACTCTTCGTCCCTGTCAATGAAGGCTTTGT  6060
1945   F  L  D  D  E  L  T  Y  K  T  L  F  V  P  V  N  E  G  F  V   1964

6061  GGACAACATGACGCTGAGTGGCCCAAACTTGGAGCTGCATGCCTCCAACGCCACCCTCCT  6120
1965   D  N  M  T  L  S  G  P  K  L  E  L  H  A  S  N  A  T  L  L   1984

6121  AAGTGCCAACGCCAGCCAGGGGAAGTTGCTTCCGGCCCACTCAGGCCTCAGCCTCATCAT  6180
1985   S  A  N  A  S  Q  G  K  L  L  P  A  H  S  G  L  S  L  I  I   2004

6181  CAGTGACGCAGGCCCTGACAACAGTTCCTGGGCCCCTGTGGCCCCAGGGACAGTTGTGGT  6240
2005   S  D  A  G  P  D  N  S  S  W  A  P  V  A  P  G  T  V  V  V   2024

6241  TAGCCGTATCATTGTGTGGGACATCATGGCCTTCAATGGCATCATCCATGCTCTGGCCAG  6300
2025   S  R  I  I  V  W  D  I  M  A  F  N  G  I  I  H  A  L  A  S   2044
```

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FIGURE 1P

```
6301  CCCCCTCCTGGCACCCCCACAGCCCCAGGCAGTGCTGGCGCNTGAAGCCCCACCTGTGGC  6360
2045   P  L  L  A  P  P  Q  P  Q  A  V  L  A  X  E  A  P  P  V  A   2064

6361  GGCAGGCGTGGGGGCTGTGCTTGCCGCTGGAGCACTGCTTGGCTTGGTGGCCGGAGCTCT  6420
2065   A  G  V  G  A  V  L  A  A  G  A  L  L  G  L  V  A  G  A  L   2084

6421  CTACCTCCGTGCCCGAGGCAAGCCCATGGGCTTTGGCTTCTCTGCCTTCCAGGCGGAAGA  6480
2085   Y  L  R  A  R  G  K  P  M  G  F  G  F  S  A  F  Q  A  E  D   2104

6481  TGATGCTGATGACGANTTCTCACCGTGGCAAGAAGGGACCAACCCCACNTTGGTNTNTGT  6540
2105   D  A  D  D  X  F  S  P  W  Q  E  G  T  N  P  T  L  V  X  V   2124

6541  CCCCAACCCTGTCTTTGGCAGCGACACCTTTTGTGAACCCTTCGATGACTCACTGCTGGA  6600
2125   P  N  P  V  F  G  S  D  T  F  C  E  P  F  D  D  S  L  L  E   2144

6601  GGAGGACTTCCCTGACACCCAGAGGATCCTCACAGTCAAGTGACGAGGCTGGGGCTGAAA  6660
2145   E  D  F  P  D  T  Q  R  I  L  T  V  K  *                     2158

6661  GCAGAAGCATGCACAGGGAGGAGACCANTTTTATTGCTTGTCTGGGTGGATGGGGCAGGA  6720

6721  GGGNCTGAGGGCCTGTCCCAGACAATANNNGTNCCCTCGAG  6761
```

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FIGURE 2A

```
                .         .         .         .         .         .
  1  GAGCACGCCAACTGTAGCCAGGTAGGAACAATGGTCACTTGTACCTGCCTGCCCGACTAC   60
  1                                  M  V  T  C  T  C  L  P  D  Y    10

                .         .         .         .         .         .
 61  GAGGGTGATGGCTGGAGCTGCCGGGCCCGCAACCCCTGCACAGATGGCCACCGCGGGGGC  120
 11  E  G  D  G  W  S  C  R  A  R  N  P  C  T  D  G  H  R  G  G    30

                .         .         .         .         .         .
121  TGCAGCGAGCACGCCAACTGCTTGAGCACCGGCCTGAACACACGGCGCTGTGAGTGCCAC  180
 31  C  S  E  H  A  N  C  L  S  T  G  L  N  T  R  R  C  E  C  H    50

                .         .         .         .         .         .
181  GCAGGCTACGTAGGCGATGGACTGCAGTGTCTGGAGGAGTCGGAACCACCTGTGGACCGC  240
 51  A  G  Y  V  G  D  G  L  Q  C  L  E  E  S  E  P  P  V  D  R    70

                .         .         .         .         .         .
241  TGCTTGGGCCAGCCACCGCCCTGCCACTCAGATGCCATGTGCACTGACCTGCACTTCCAG  300
 71  C  L  G  Q  P  P  P  C  H  S  D  A  M  C  T  D  L  H  F  Q    90

                .         .         .         .         .         .
301  GAGAAACGGGCTGGCGTTTTCCACCTCCAGGCCACCAGCGGCCCTTATGGTCTGAACTTT  360
 91  E  K  R  A  G  V  F  H  L  Q  A  T  S  G  P  Y  G  L  N  F   110

                .         **********************************************
361  TCGGAGGCTGAGGCGGCATGCGAAGCACAGGGAGCCGTCCTTGCTTCATTCCCTCAGCTC  420
111  S  E  A  E  A  A  C  E  A  Q  G  A  V  L  A  S  F  P  Q  L   130
```

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FIGURE 2B

```
                **************************************************************
421  TCTGCTGCCCAGCAGCTGGGCTTCCACCTGTGCCTCATGGGCTGGCTGGCCAATGGCTCC   480
131  S  A  A  Q  Q  L  G  F  H  L  C  L  M  G  W  L  A  N  G  S    150

                ***********************************
481  ACTGCCCACCCTGTGGTTTTCCCTGTGGCGGACTGTGGCAATGGTCGGGTGGGCATAGTC   540
151  T  A  H  P  V  V  F  P  V  A  D  C  G  N  G  R  V  G  I  V    170

541  AGCCTGGGTGCCCGCAAGAACCTCTCAGAACGCTGGGATGCCTACTGCTTCCGTGTGCAA   600
171  S  L  G  A  R  K  N  L  S  E  R  W  D  A  Y  C  F  R  V  Q    190

601  GATGTGGCCTGCCGATGCCGAAATGGCTTCGTGGGTGACGGGATCAGCACGTGCAATGGG   660
191  D  V  A  C  R  C  R  N  G  F  V  G  D  G  I  S  T  C  N  G    210

661  AAGCTGCTGGATGTGCTGGCTGCCACTGCCAACTTCTCCACCTTCTATGGGATGCTATTG   720
211  K  L  L  D  V  L  A  A  T  A  N  F  S  T  F  Y  G  M  L  L    230

721  GGCTATGCCAATGCCACCCAGCGGGGTCTCGACTTCCTGGACTTCCTGGATGATGAGCTC   780
231  G  Y  A  N  A  T  Q  R  G  L  D  F  L  D  F  L  D  D  E  L    250

781  ACGTATAAGACACTCTTCGTCCCTGTCAATGAAGGCTTTGTGGACAACATGACGCTGAGT   840
251  T  Y  K  T  L  F  V  P  V  N  E  G  F  V  D  N  M  T  L  S    270
```

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FIGURE 2C

```
                .         .         .         .         .         .
841  GGCCCAAACTTGGAGCTGCATGCCTCCAACGCCACCCTCCTAAGTGCCAACGCCAGCCAG   900
271  G  P  N  L  E  L  H  A  S  N  A  T  L  L  S  A  N  A  S  Q    290

                .         .         .         .         .         .
901  GGGAAGTTGCTTCCGGCCCACTCAGGCCTCAGCCTCATCATCAGTGACGCAGGCCCTGAC   960
291  G  K  L  L  P  A  H  S  G  L  S  L  I  I  S  D  A  G  P  D    310

                .         .         .         .         .         .
961  AACAGTTCCTGGGCCCCTGTGGCCCCAGGGACAGTTGTGGTTAGCCGTATCATTGTGTGG   1020
311  N  S  S  W  A  P  V  A  P  G  T  V  V  V  S  R  I  I  V  W    330

                .         .         .         .         .         .
1021 GACATCATGGCCTTCAATGGCATCATCCATGCTCTGGCCAGCCCCCTCCTGGCACCCCCA   1080
331  D  I  M  A  F  N  G  I  I  H  A  L  A  S  P  L  L  A  P  P    350

                .         .         .         .         .         .
1081 CAGCCCCAGGCAGTGCTGGCGCNTGAAGCCCCACCTGTGGCGGCAGGCGTGGGGGCTGTG   1140
351  Q  P  Q  A  V  L  A  X  E  A  P  P  V  A  A  G  V  G  A  V    370

                .         .         .         .         .         .
1141 CTTGCCGCTGGAGCACTGCTTGGCTTGGTGGCCGGAGCTCTCTACCTCCGTGCCCGAGGC   1200
371  L  A  A  G  A  L  L  G  L  V  A  G  A  L  Y  L  R  A  R  G    390

                .         .         .         .         .         .
1201 AAGCCCATGGGCTTTGGCTTCTCTGCCTTCCAGGCGGAAGATGATGCTGATGACGANTTC   1260
391  K  P  M  G  F  G  F  S  A  F  Q  A  E  D  D  A  D  D  X  F    410
```

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FIGURE 2D

```
                .         .         .         .         .         .
1261  TCACCGTGGCAAGAAGGGACCAACCCCACNTTGGTNTNTGTCCCCAACCCTGTCTTTGGC  1320
 411  S  P  W  Q  E  G  T  N  P  T  L  V  X  V  P  N  P  V  F  G    430

                .         .         .         .         .         .
1321  AGCGACACCTTTTGTGAACCCTTCGATGACTCACTGCTGGAGGAGGACTTCCCTGACACC  1380
 431  S  D  T  F  C  E  P  F  D  D  S  L  L  E  E  D  F  P  D  T    450

                .         .         .         .         .         .
1381  CAGAGGATCCTCACAGTCAAGTGACGAGGCTGGGGCTGAAAGCAGAAGCATGCACAGGGA  1440
 451  Q  R  I  L  T  V  K  *                                        458

                .         .         .         .         .         .
1441  GGAGACCANTTTTATTGCTTGTCTGGGTGGATGGGGCAGGAGGGNCTGAGGGCCTGTCCC  1500

                .         .
1501  AGACAATANNNGTNCCCTCGAG  1522
```

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FIGURE 3A

```
  1  GCCCACGCGTCCGACCGGGACAGCTCGCGGCCCCCNAGAGCTCTAGCCGTNGAGGAGCTG   60

 61  CCTGGGGACGTTTGCCCTGGGGCCCCAGCCTGGCCCGGGTCACCCTGGCATGAGGAGATG  120
  1                                                          M     1

121  GGCCTGTTGCTCCTGGTCCCATTGCTCCTGCTGCCCGGCTCCTACGGACTGCCCTTCTAC  180
  2  G  L  L  L  L  V  P  L  L  L  L  P  G  S  Y  G  L  P  F  Y    21

181  TACGGCTTCTACTACTCCAACAGCGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAA  240
 22  Y  G  F  Y  Y  S  N  S  A  N  D  Q  N  L  G  N  G  H  G  K    41

241  GACCTACNTAATGGAGTGAAGCTGGTGGTGGAGACACCCGAGGAGACCCTGTTCACCTAC  300
 42  D  L  X  N  G  V  K  L  V  V  E  T  P  E  E  T  L  F  T  Y    61

301  CAAGGGGCCAGTGTGATCCTGCCCTGCCGCTACCGCTACGAGCCGGCCCTGGTCTCCCCG  360
 62  Q  G  A  S  V  I  L  P  C  R  Y  R  Y  E  P  A  L  V  S  P    81

361  CGGCGTGTGCGTGTCAAATGGTGGAAGCTGTCGGAGAACGGGGCCCCAGAGAAGGACGTG  420
 82  R  R  V  R  V  K  W  W  K  L  S  E  N  G  A  P  E  K  D  V   101
```

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FIGURE 3B

```
421  CTGGTGGCCATCGGGCTGAGGCACCGCTCCTTTGGGGACTACCAAGGCCGCGTGCACCTG  480
102  L  V  A  I  G  L  R  H  R  S  F  G  D  Y  Q  G  R  V  H  L    121

481  CGGCAGGACAAAGAGCATGACGTCTCGNTGGAGATCCAGGNTCTGCGGCTGGAGGACTAT  540
122  R  Q  D  K  E  H  D  V  S  X  E  I  Q  X  L  R  L  E  D  Y    141

541  GGGCGTTACCGCTGTGAGGTCATNGACGGGCTGGAGGATGAAAGCGGTCTGGTGGAGCTG  600
142  G  R  Y  R  C  E  V  X  D  G  L  E  D  E  S  G  L  V  E  L    161

601  GAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCAACGGGCGCTACCAGTTCAACTTC  660
162  E  L  R  G  V  V  F  P  Y  Q  S  P  N  G  R  Y  Q  F  N  F    181

     **********************************************
661  CACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTGGTGGCCTCCTTTGAGCAGCTC  720
182  H  E  G  Q  Q  V  C  A  E  Q  A  A  V  V  A  S  F  E  Q  L    201

     ************************************************************
721  TTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGGCTGGCTGCAGGATGCCACG  780
202  F  R  A  W  E  E  G  L  D  W  C  N  A  G  W  L  Q  D  A  T    221

     ***********************************
781  GTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCGGTGGCCCGGACCTGGCACCTGGC  840
222  V  Q  Y  P  I  M  L  P  R  Q  P  C  G  G  P  D  L  A  P  G    241
```

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FIGURE 3C

```
841  GTGCGAAGCTACGGCCCCCGCCACCGCCGCCTGCACCGCTATGATGTATTCTGCTTCGCT  900
242  V  R  S  Y  G  P  R  H  R  R  L  H  R  Y  D  V  F  C  F  A    261

901  ACTGCCCTCARGGGGCGGGTGTACTACCTGGANCACCCTGAGAANCTGACNCTGACANAA  960
262  T  A  L  X  G  R  V  Y  Y  L  X  H  P  E  X  L  T  L  T  X  281

961  GCAAGGGAAGCCTGCCAAGAAAAAT  985
282  A  R  E  A  C  Q  E  K    289
```

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FIGURE 4A

```
   1  GGAATCACATGCACAGTTGTGGATTTYTGCAAACAGGACAACGGGGGCTGTGCAAAGGTG   60

  61  GCCAGATGCTCCCAGAAGGGCACGAAGGTCTCCTGCAGCTGCCAGAAGGGATACAAAGGG  120

 121  GACGGGCACAGCTGCACAGAGATAGACCCCTGTGCAGACGGCCTTAACGGAGGGTGTCAC  180

 181  GAGCACGCCACCTGTAAGATGACAGGCCCGGGCAAGCACAAGTGTGAGTGTAAAAGTCAC  240
   1                  M  T  G  P  G  K  H  K  C  E  C  K  S  H      14

 241  TATGTCGGAGATGGGCTGAACTGTGAGCCGGAGCAGCTGCCCATTGACCGCTGCTTACAG  300
  15  Y  V  G  D  G  L  N  C  E  P  E  Q  L  P  I  D  R  C  L  Q   34

 301  GACAATGGGCAGTGCCATGCAGACGCCAAATGTGTCGACCTCCACTTCCAGGATACCACT  360
  35  D  N  G  Q  C  H  A  D  A  K  C  V  D  L  H  F  Q  D  T  T   54

 361  GTTGGGGTGTTCCATCTACGCTCCCCACTGGGCCAGTATAAGCTGACCTTTGACAAAGCC  420
  55  V  G  V  F  H  L  R  S  P  L  G  Q  Y  K  L  T  F  D  K  A   74

 421  AGAGAGGCCTGTGCCAACGAAGCTGCGACCATGGCAACCTACAACCAGCTCTCCTATNNC  480
  75  R  E  A  C  A  N  E  A  A  T  M  A  T  Y  N  Q  L  S  Y  X   94
```

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FIGURE 4B

```
481  CAGAAGGCCAAGTACCACCTGTGCTCAGCAGGCTGGCTGGAGACCGGGCGGGTTGCCTAC  540
 95  Q  K  A  K  Y  H  L  C  S  A  G  W  L  E  T  G  R  V  A  Y    114

541  CCCACAGCCTTCGCCTCCCAGAACTGTGGCTCTGGTGTGGTTGGGATAGTGGACTATGGA  600
115  P  T  A  F  A  S  Q  N  C  G  S  G  V  V  G  I  V  D  Y  G    134

601  CCTAGACCCAACAAGAGTGAAATGTGGGATGTCTTCTGCTATCGGATGAAAGATGTGAAC  660
135  P  R  P  N  K  S  E  M  W  D  V  F  C  Y  R  M  K  D  V  N    154

661  TGCACCTNCAAGGTGGGCTATGTGGGAGATGGCTTCTCATACAGTGGGAACCTGCTGCAG  720
155  C  T  X  K  V  G  Y  V  G  D  G  F  S  Y  S  G  N  L  L  Q    174

721  GTCCTGATGTCCTTCCCCTCACTCACAAACTTCCTGACGGAAGTGCTGGCCTATTCCAAC  780
175  V  L  M  S  F  P  S  L  T  N  F  L  T  E  V  L  A  Y  S  N    194

781  AGCTCAGCTCGAGGCCGTGCATTTCTAGAACACCTGACTGACCTGTCCATCCGCGGCACC  840
195  S  S  A  R  G  R  A  F  L  E  H  L  T  D  L  S  I  R  G  T    214
```

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FIGURE 4C

```
                .         .         .         .         .         .
841  CTCTTTGTNCCACAGAACAGTGGGCTGGGGGAGAATGAGACCTTGTCTGGGCGGGACATC  900
215  L  F  V  P  Q  N  S  G  L  G  E  N  E  T  L  S  G  R  D  I   234

                .         .         .         .         .         .
901  GAGCACCACCTCGCCAATGTCAGCATGTTTTTCTACAATGACCTTGTCAATGGCACCACC  960
235  E  H  H  L  A  N  V  S  M  F  F  Y  N  D  L  V  N  G  T  T   254

                .         .         .         .         .         .
961  CTGCAAACGAGGCTGGGAAGCAAGCTGCTCATCACTGACAGACAGGACCCACTCCACCCG  1020
255  L  Q  T  R  L  G  S  K  L  L  I  T  D  R  Q  D  P  L  H  P   274

                .         .         .         .         .         .
1021 ACGGAGACCAGGTGTGTTGATGGAAGAGACACTCTGGAGTGGGACATCTGTGCCTCCAAT  1080
275  T  E  T  R  C  V  D  G  R  D  T  L  E  W  D  I  C  A  S  N   294

                .         .         .         .         .         .
1081 GGGATCACACATGTCATTTCCAGGYCTTTAAAAGCACCCCCTGCCCCCGTGACCTTGNCC  1140
295  G  I  T  H  V  I  S  R  X  L  K  A  P  P  A  P  V  T  L  X   314

                .         .         .         .         .         .
1141 CACACTGGNTTGGGAGNAGGGATCTTCTNTGNCATCATCCTGGTGACTGGGGCTGTTGCC  1200
315  H  T  G  L  G  X  G  I  F  X  X  I  I  L  V  T  G  A  V  A   334

                .         .         .         .         .
1201 TTGGCTGCTTACTCCTACTTTCGGATAAACCGGAAAACAATCGGCTTCCANCATTTTGA  1259
335  L  A  A  Y  S  Y  F  R  I  N  R  K  T  I  G  F  X  H  F      353
```

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FIGURE 5A

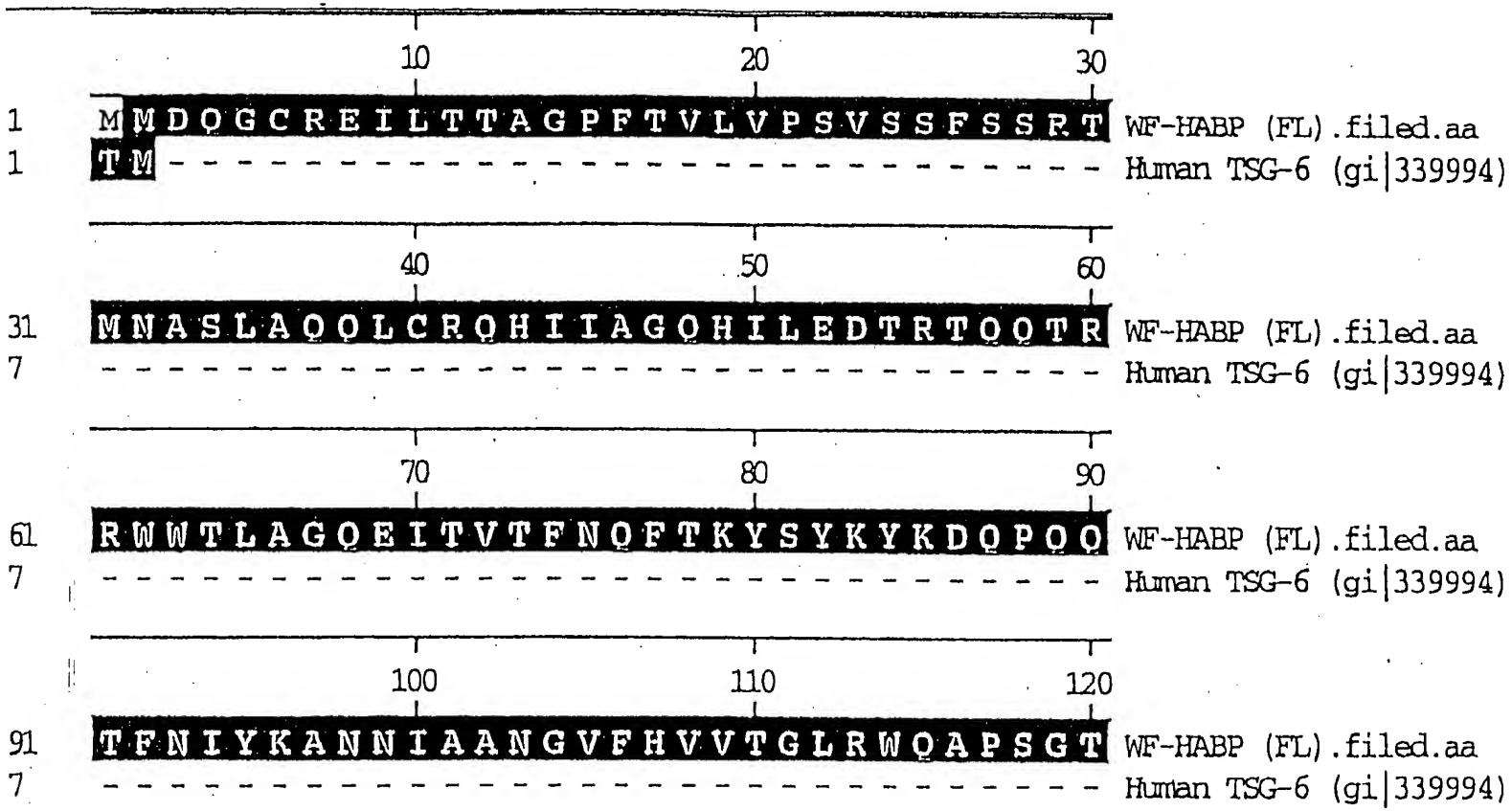

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FIGURE 5B

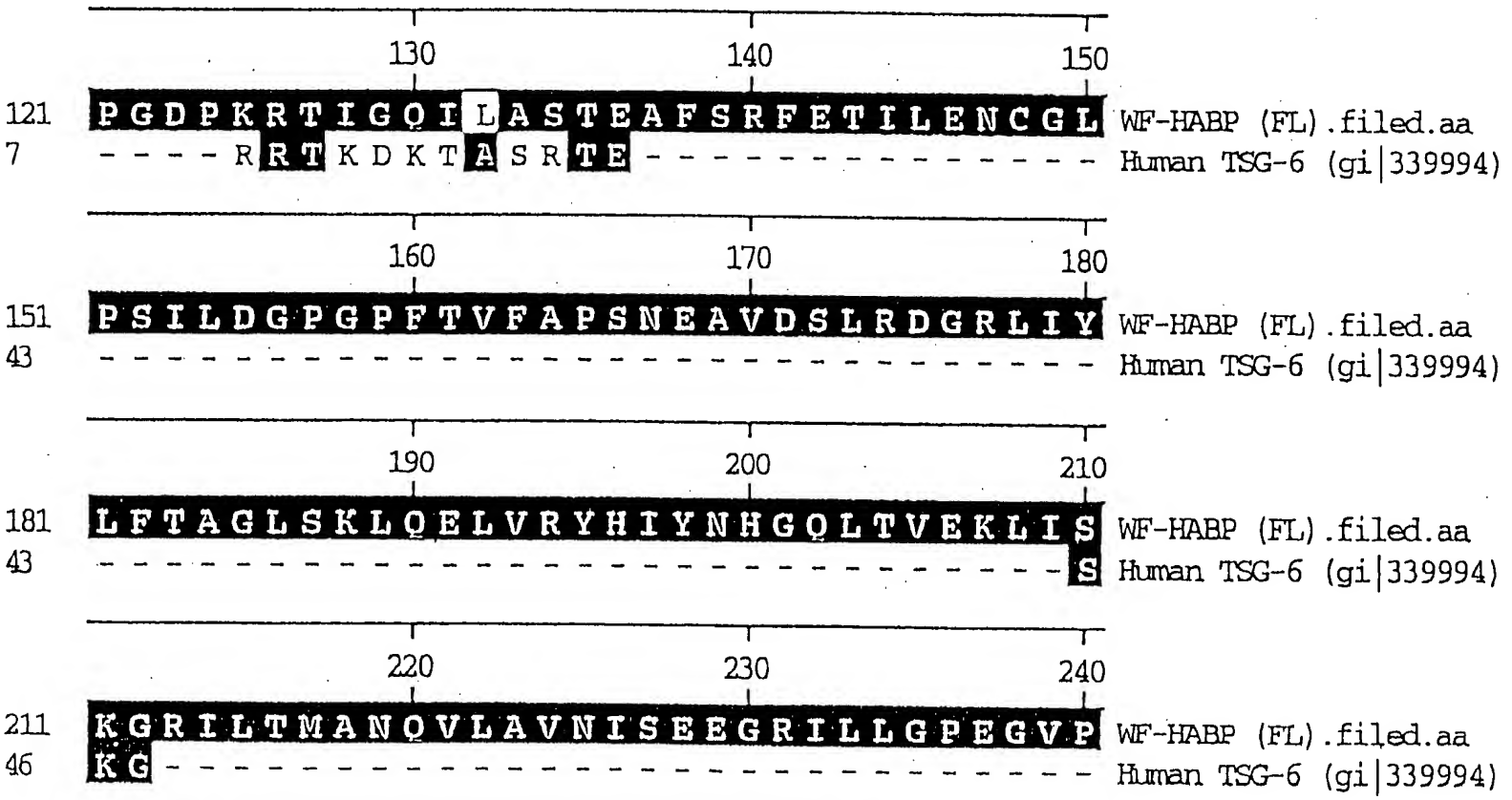

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FIGURE 5C

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FIGURE 5D

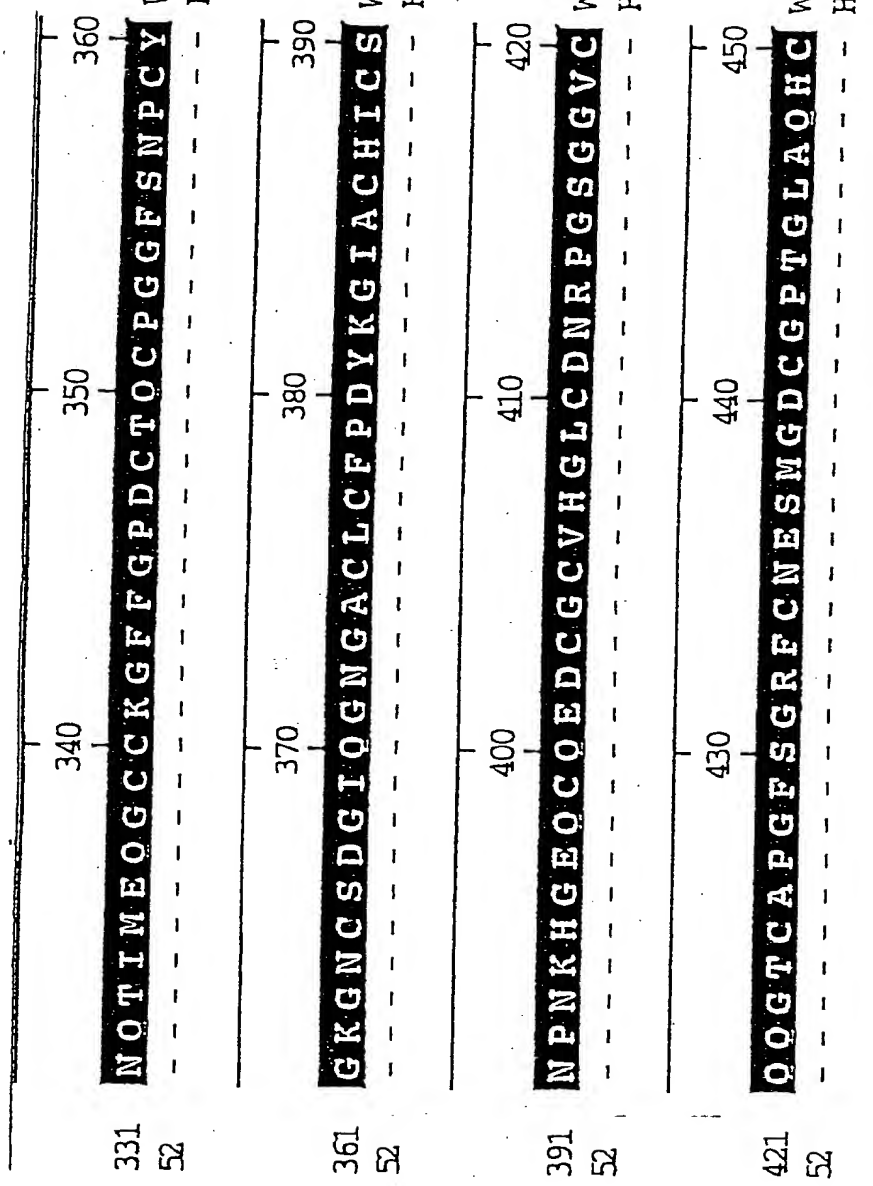

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FIGURE 5E

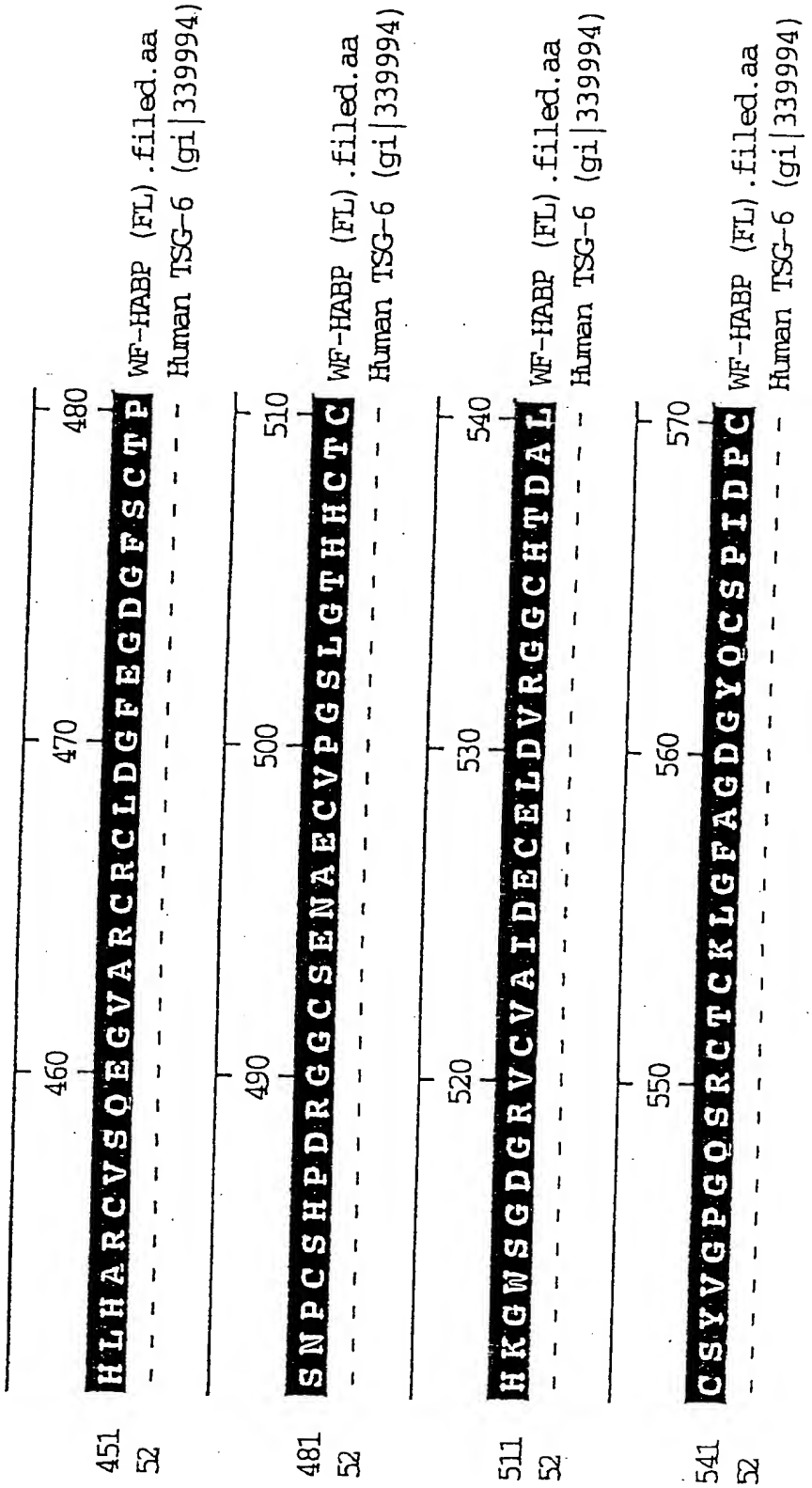

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FIGURE 5F

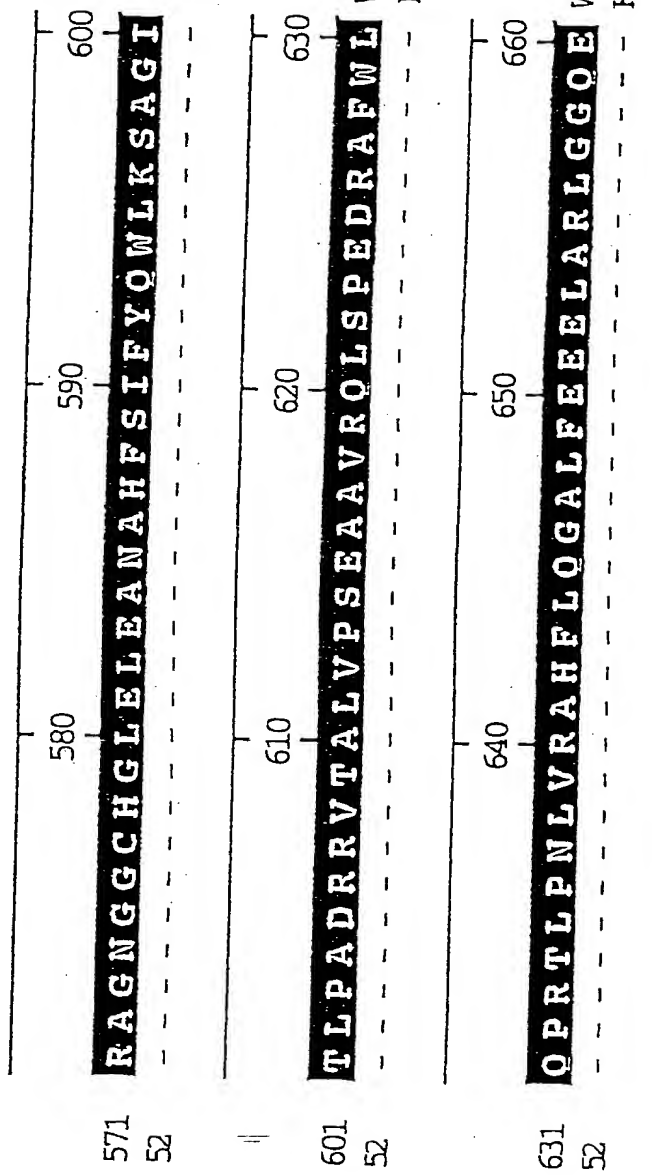

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FIGURE 5G

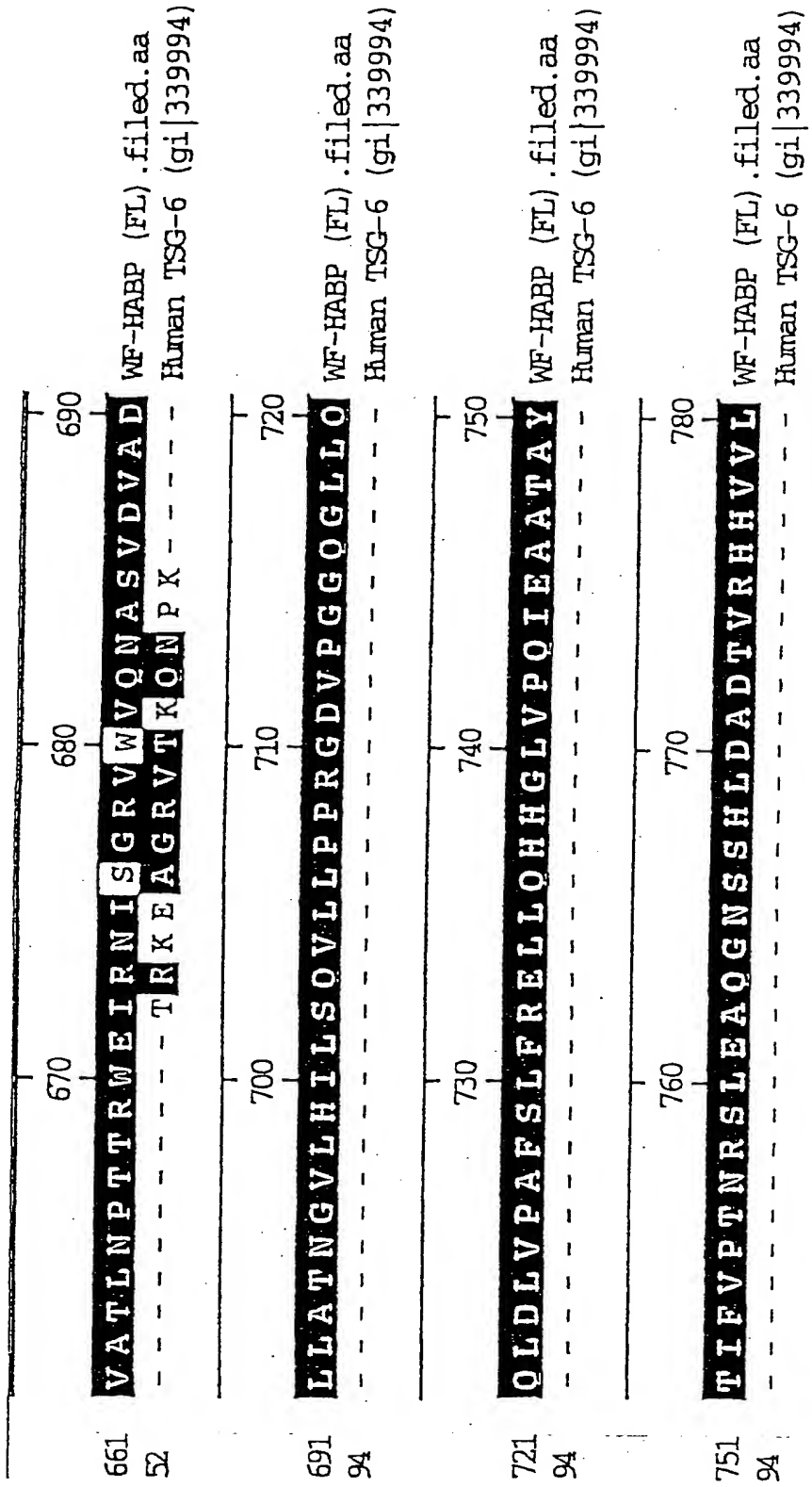

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FIGURE 5H

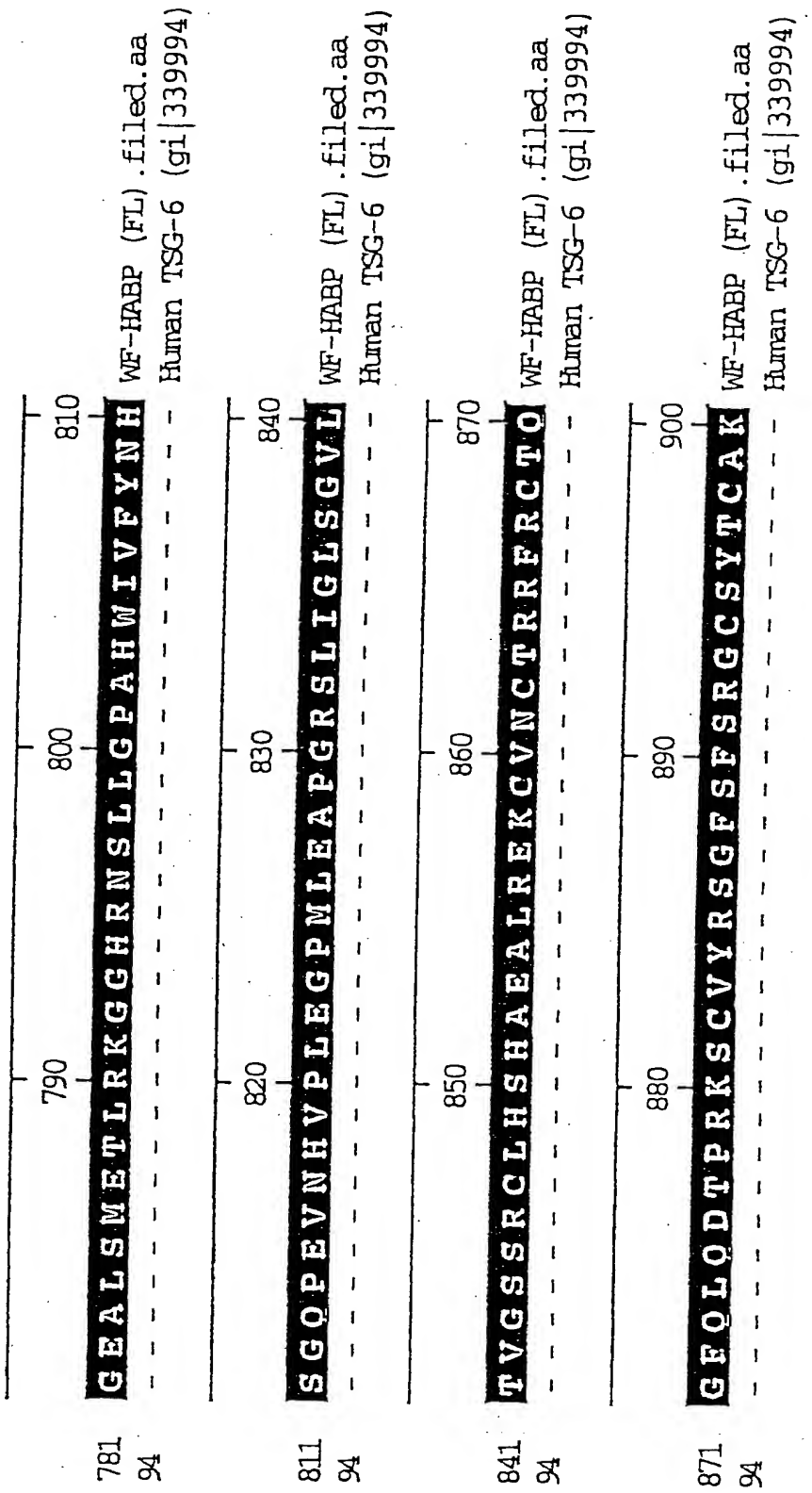

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FIGURE 5I

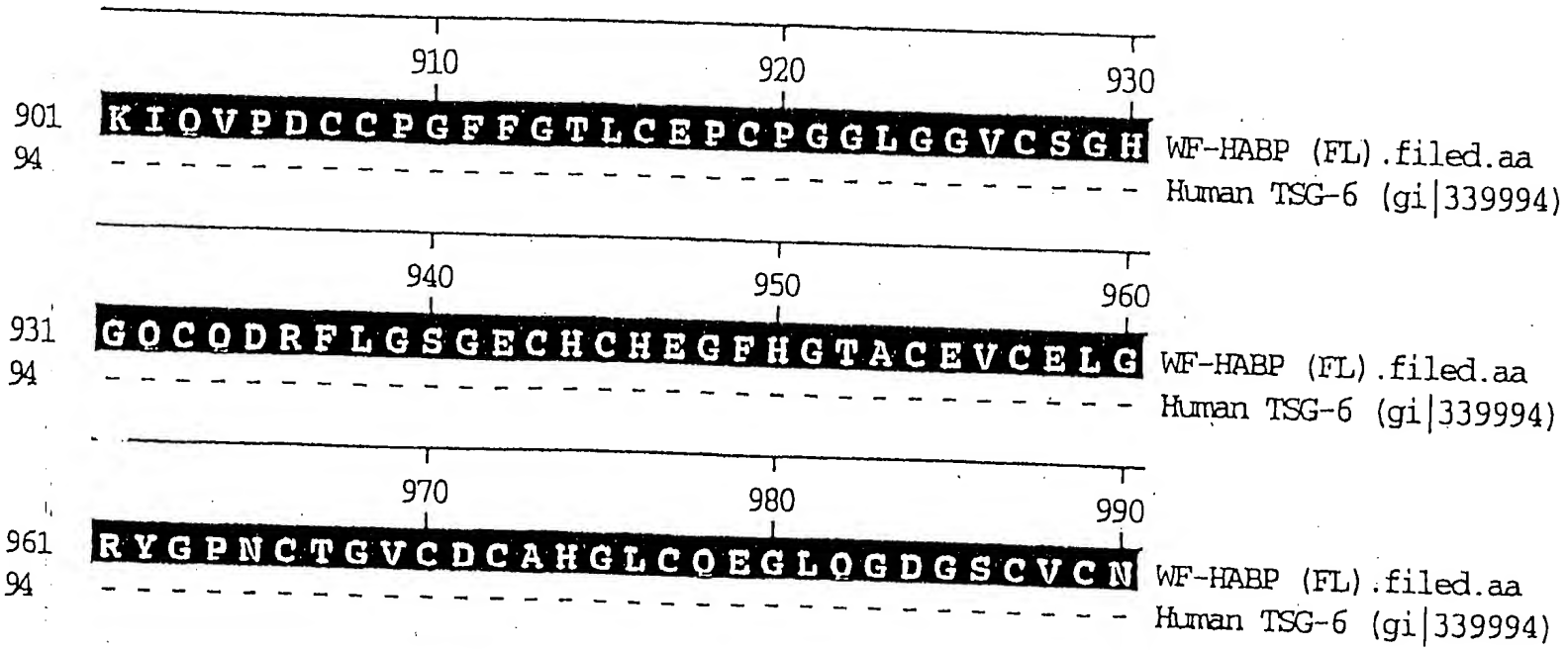

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FIGURE 5J

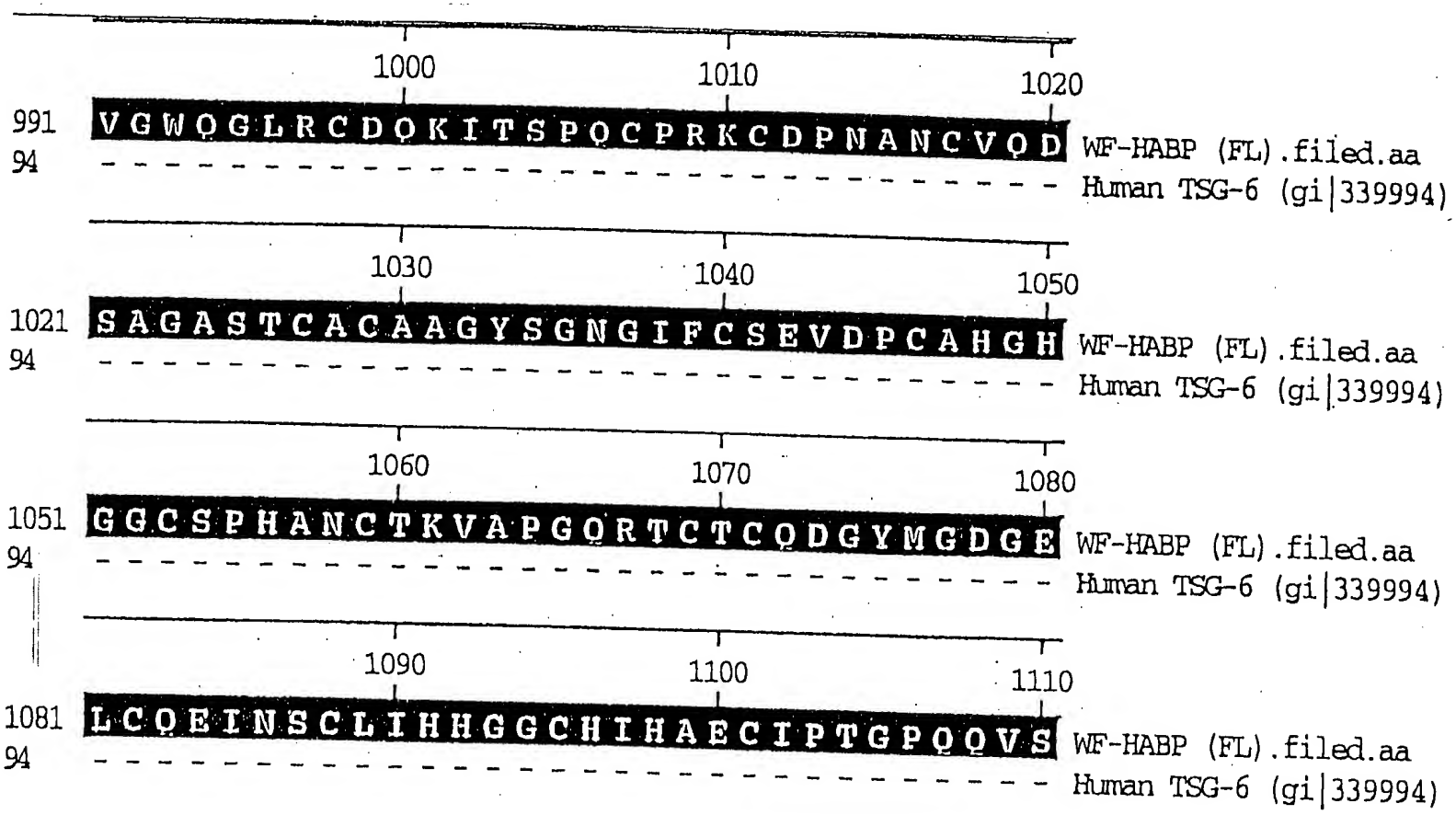

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FIGURE 5K

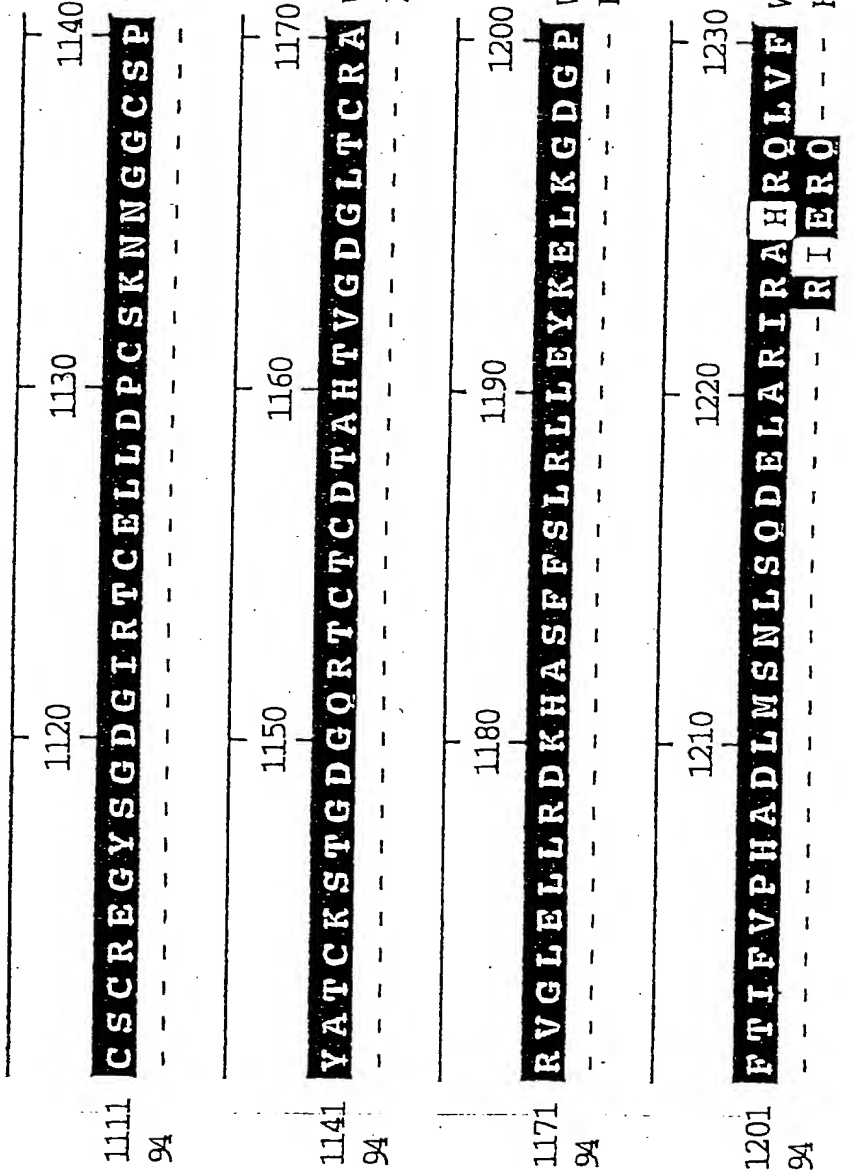

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FIGURE 5L

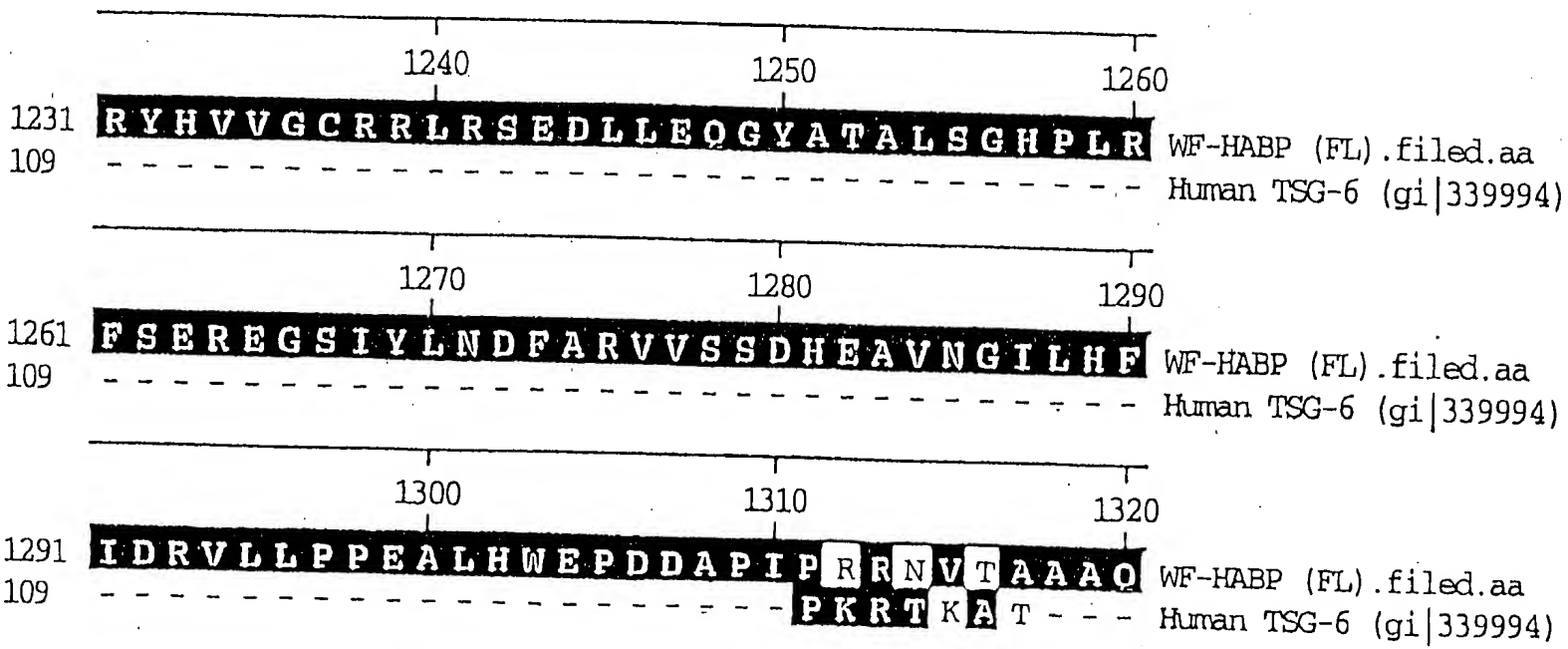

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FIGURE 5M

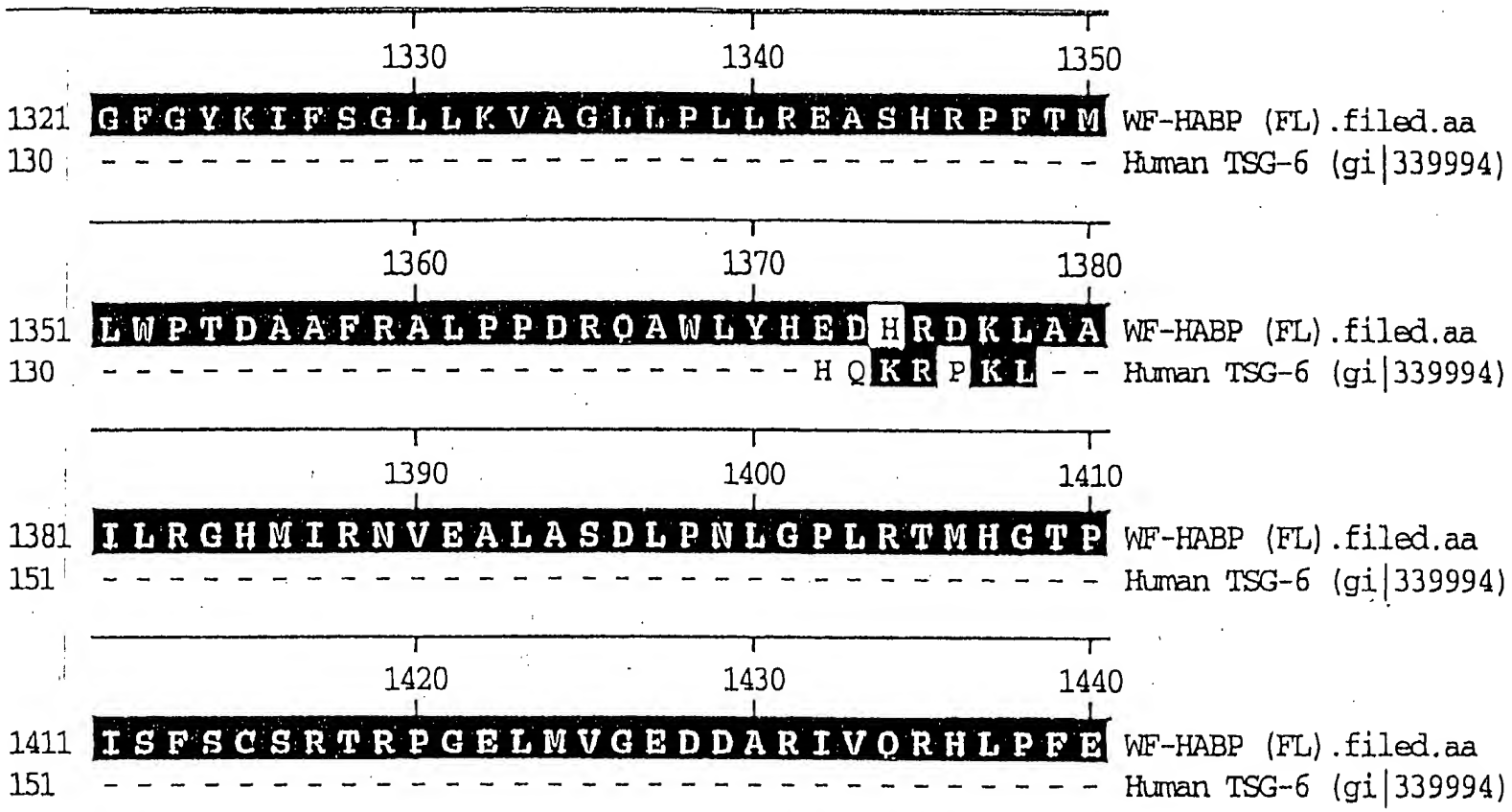

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FIGURE 5N

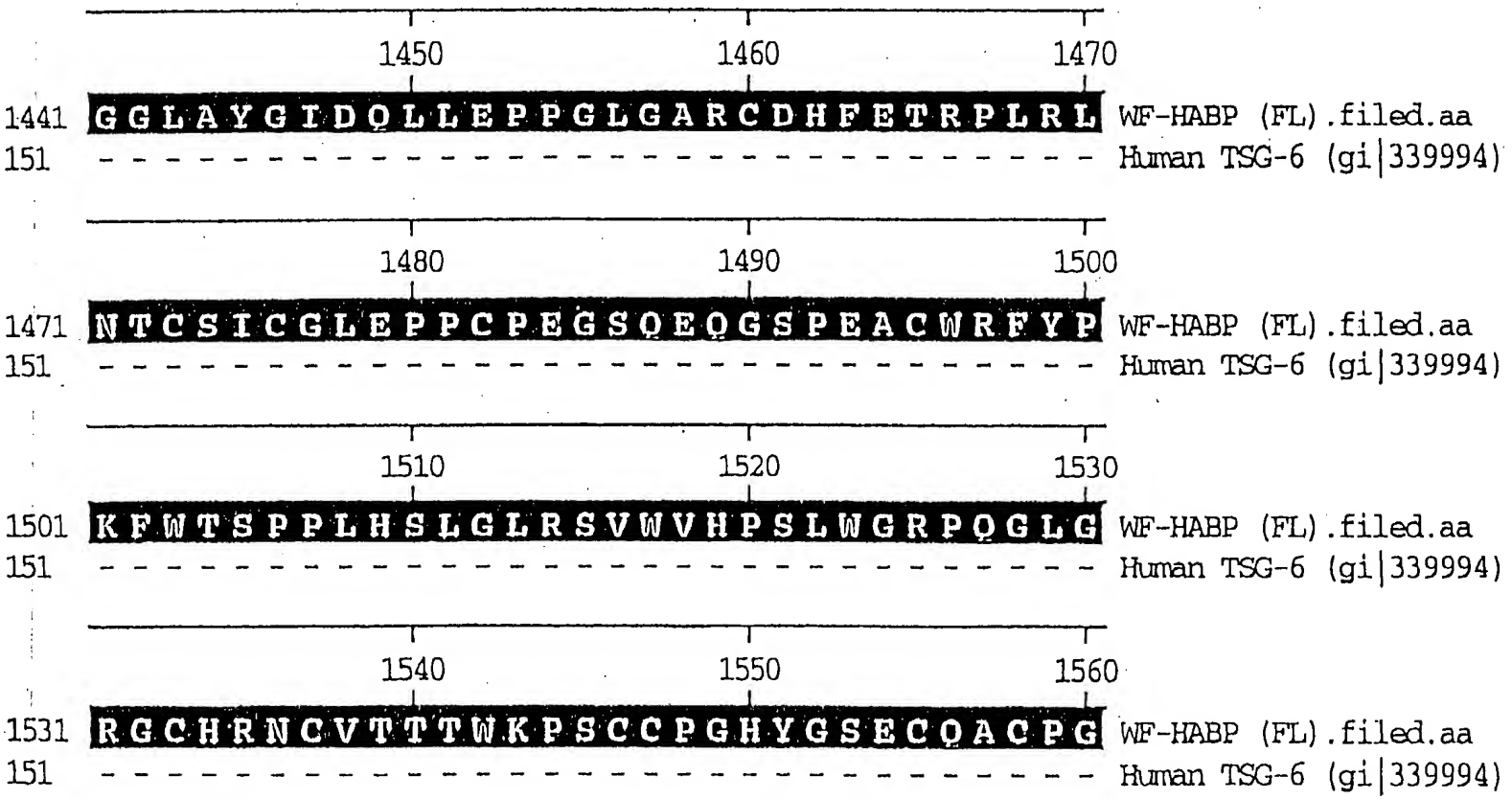

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FIGURE 5O

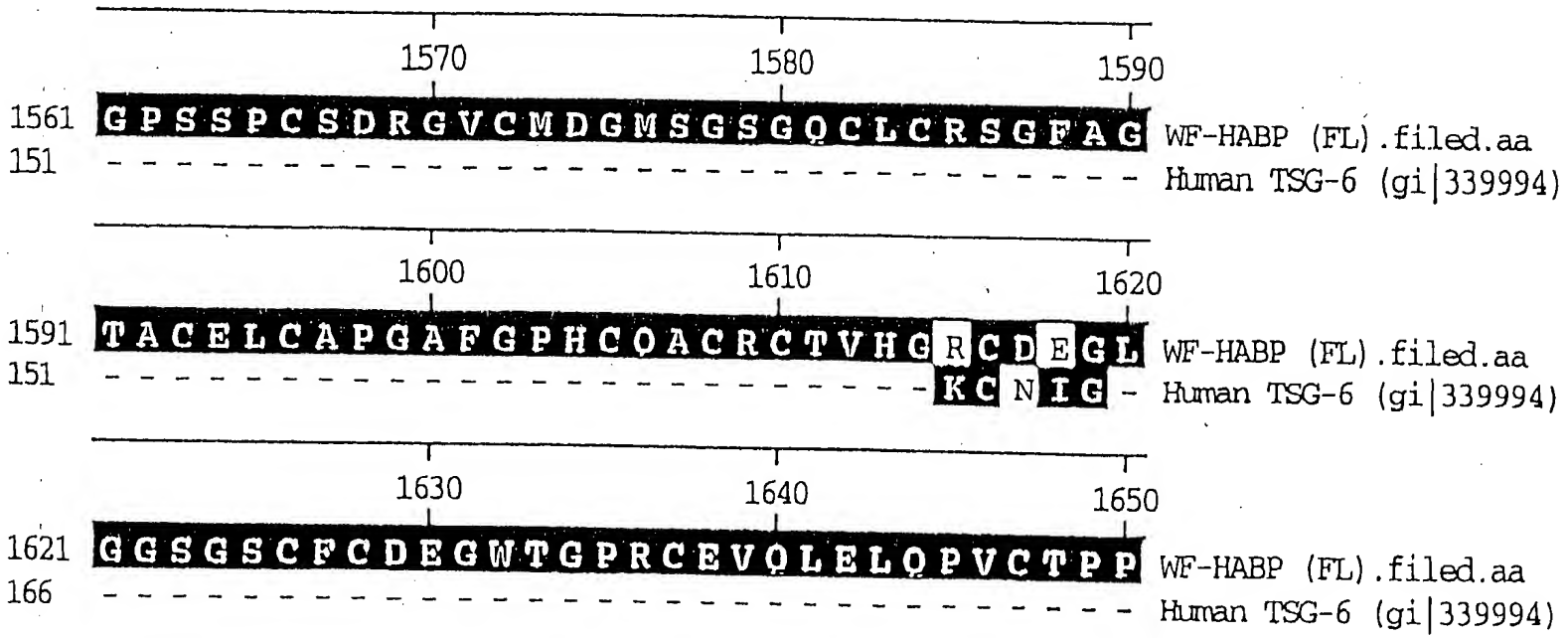

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FIGURE 5P

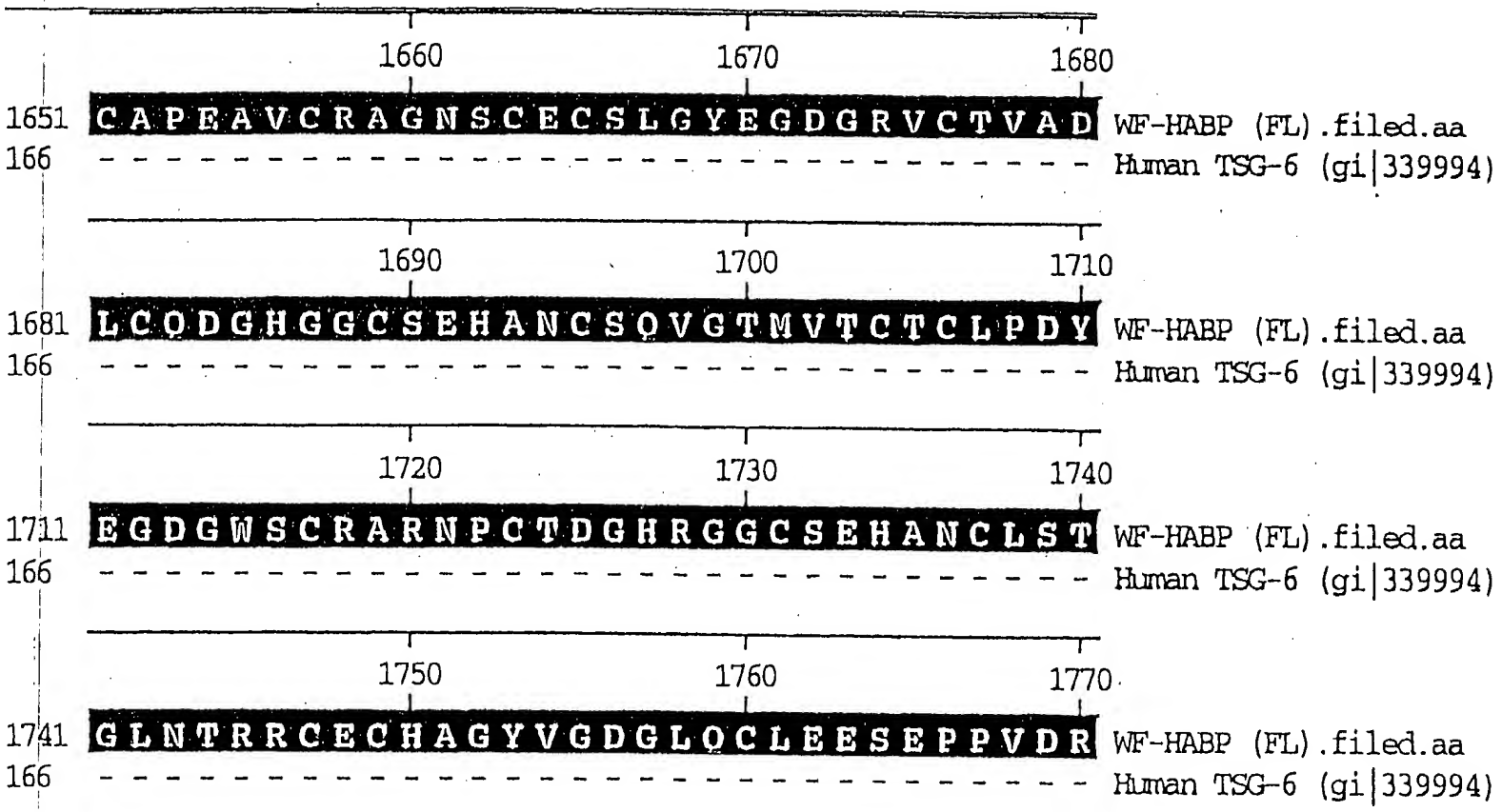

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FIGURE 5Q

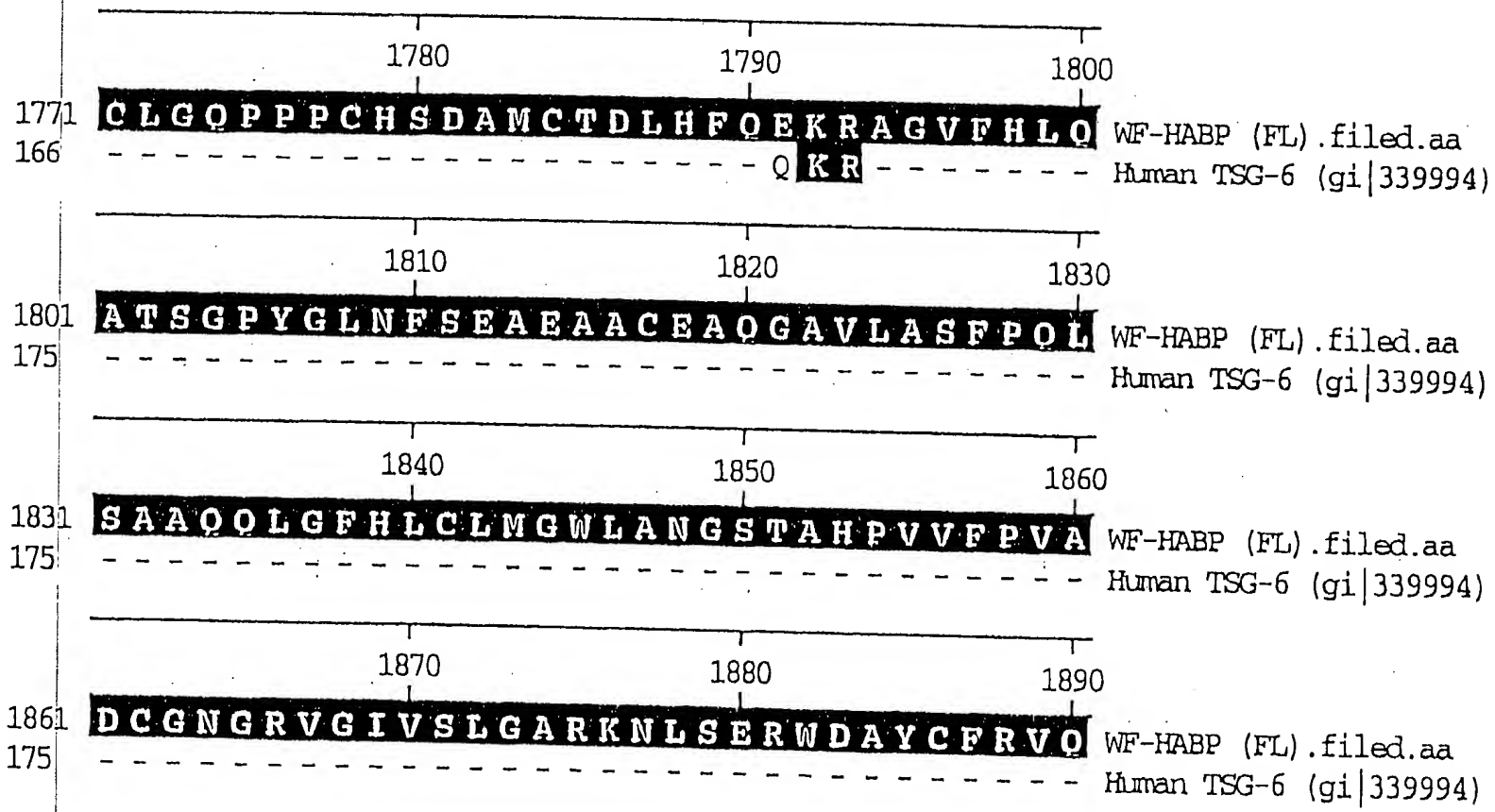
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FIGURE 5R

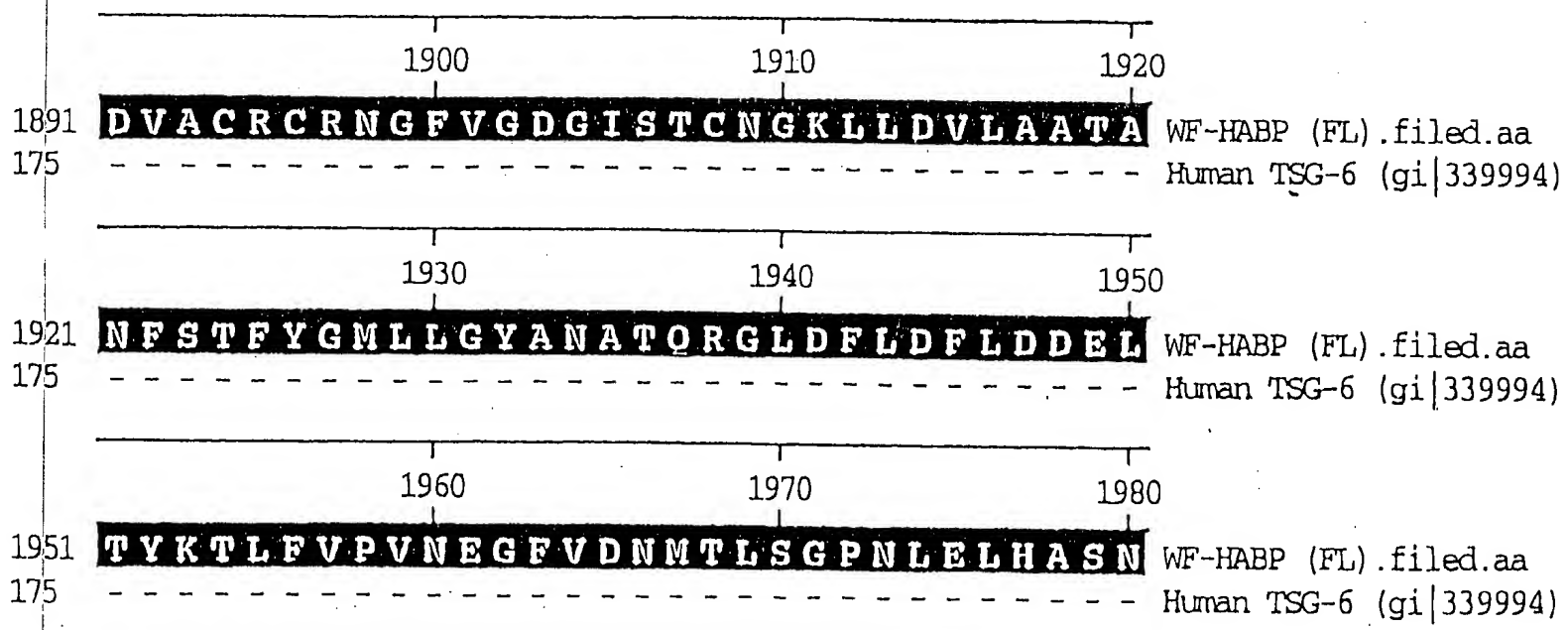
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FIGURE 5S

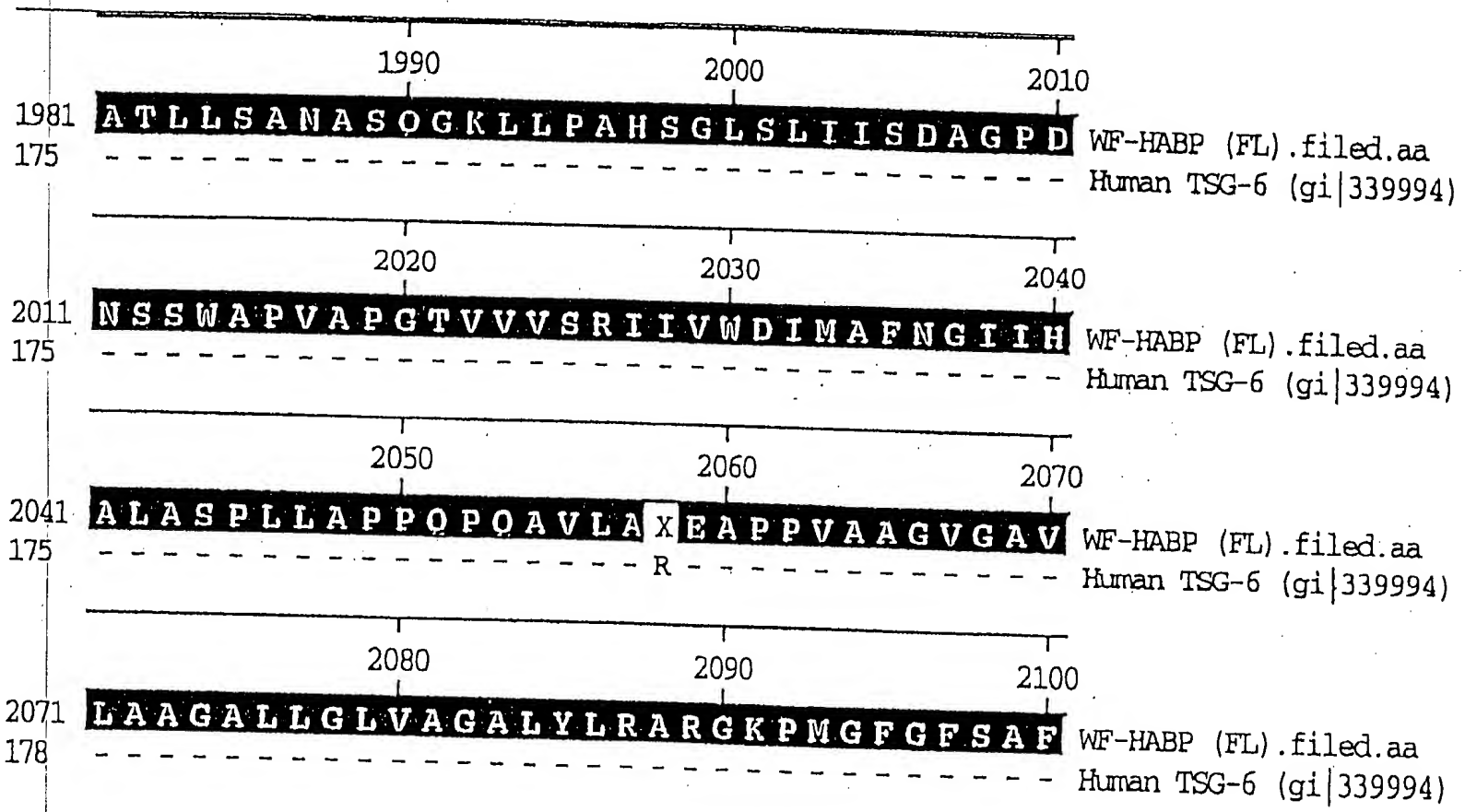

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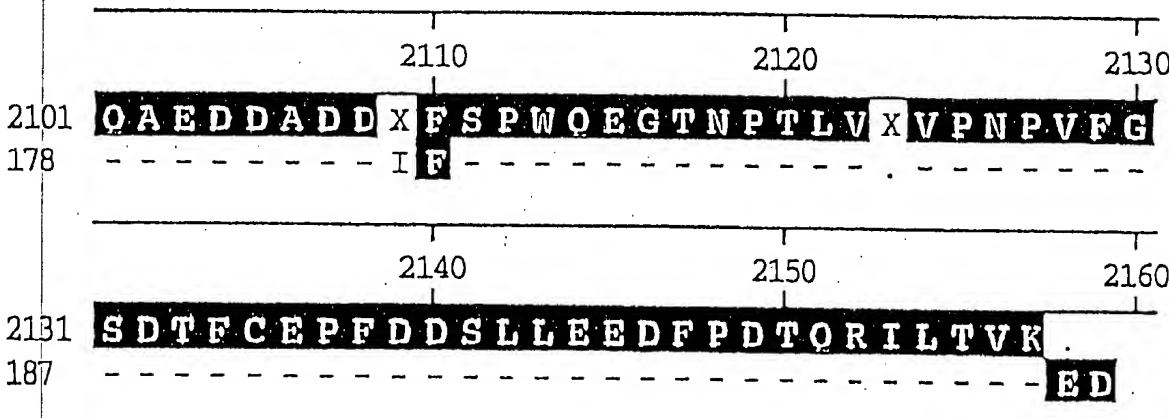
FIGURE 5T



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

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FIGURE 6A

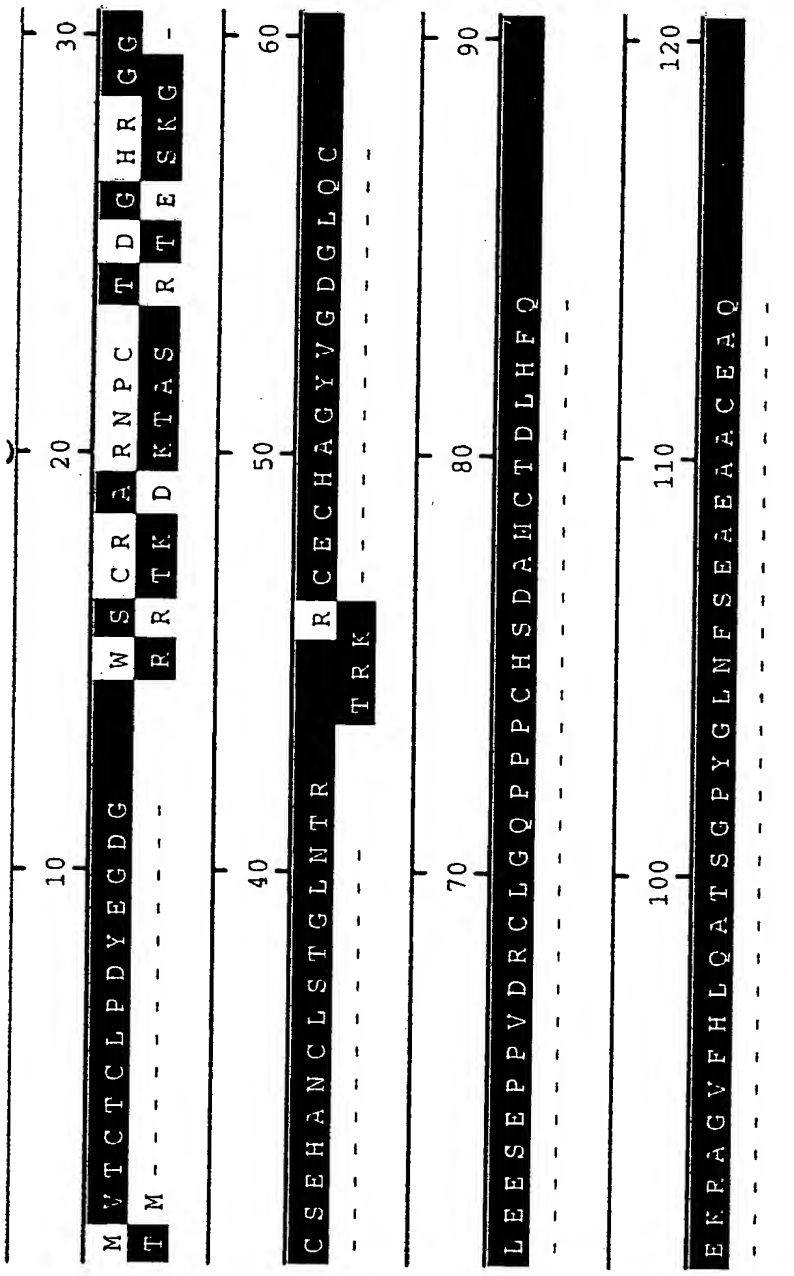

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FIGURE 6B

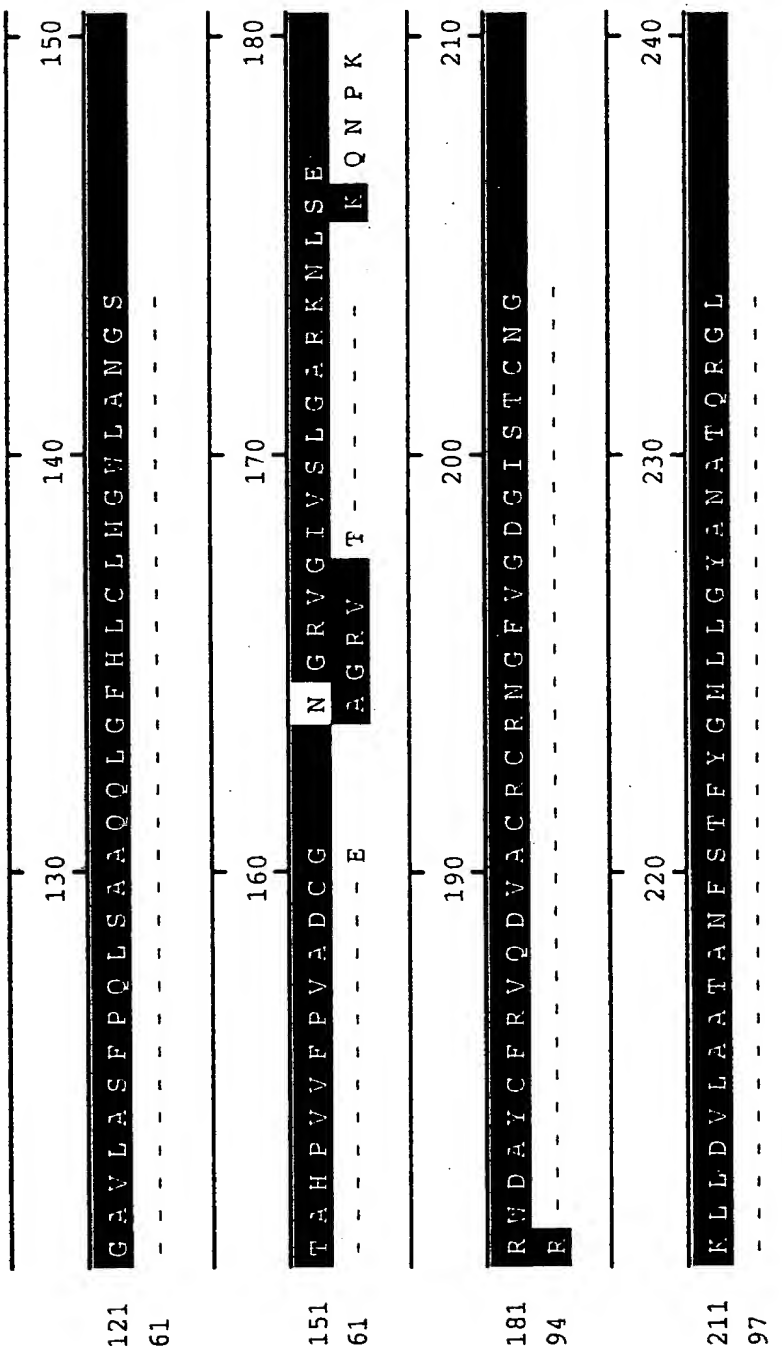

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FIGURE 6C

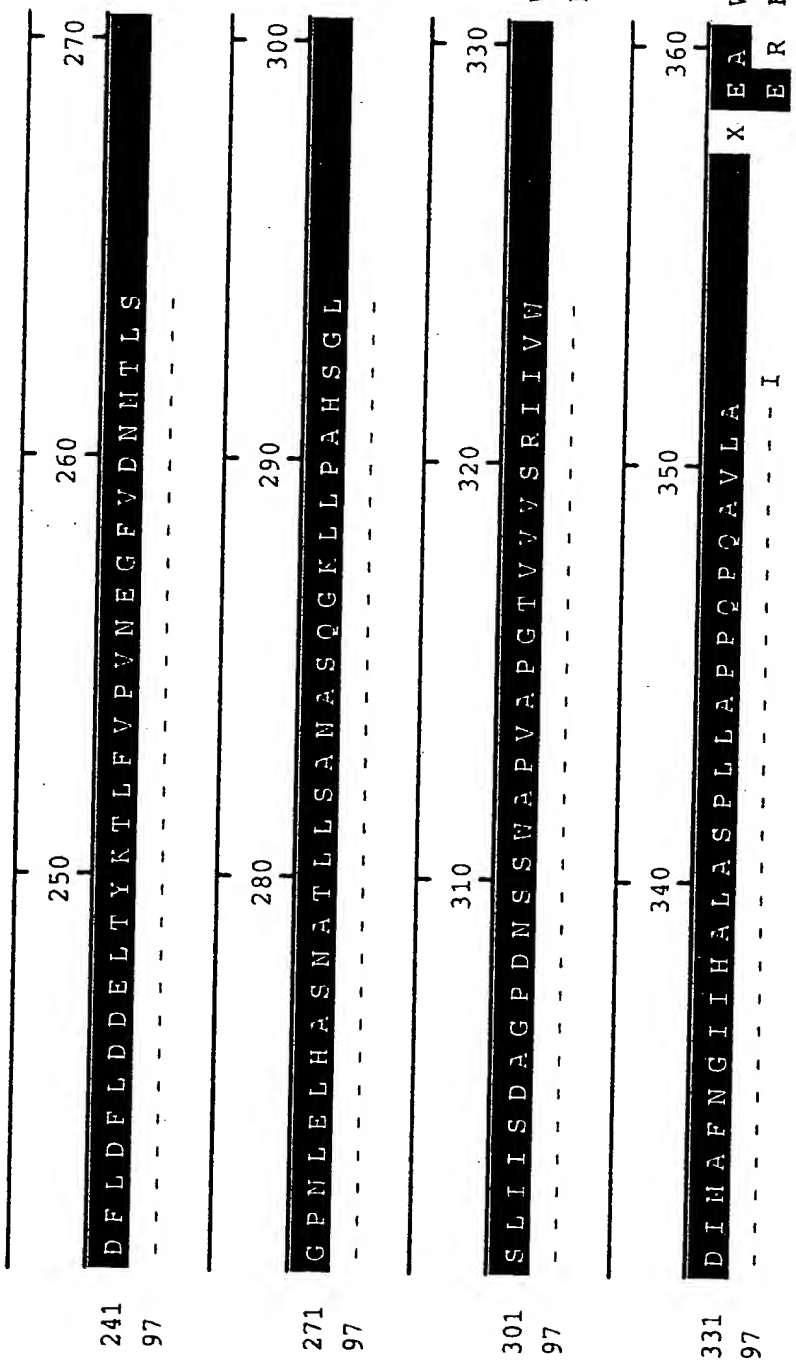

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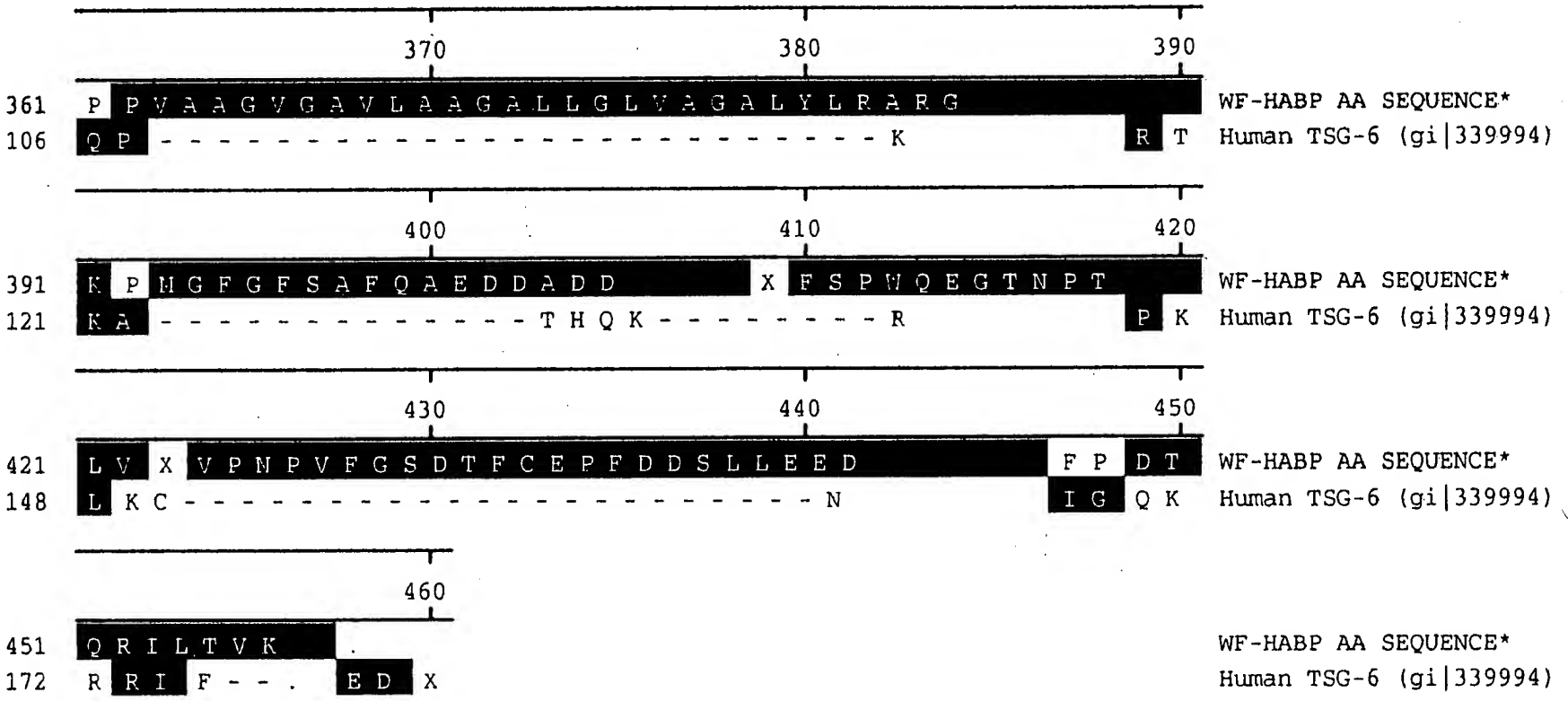
FIGURE 6D



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

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FIGURE 7A

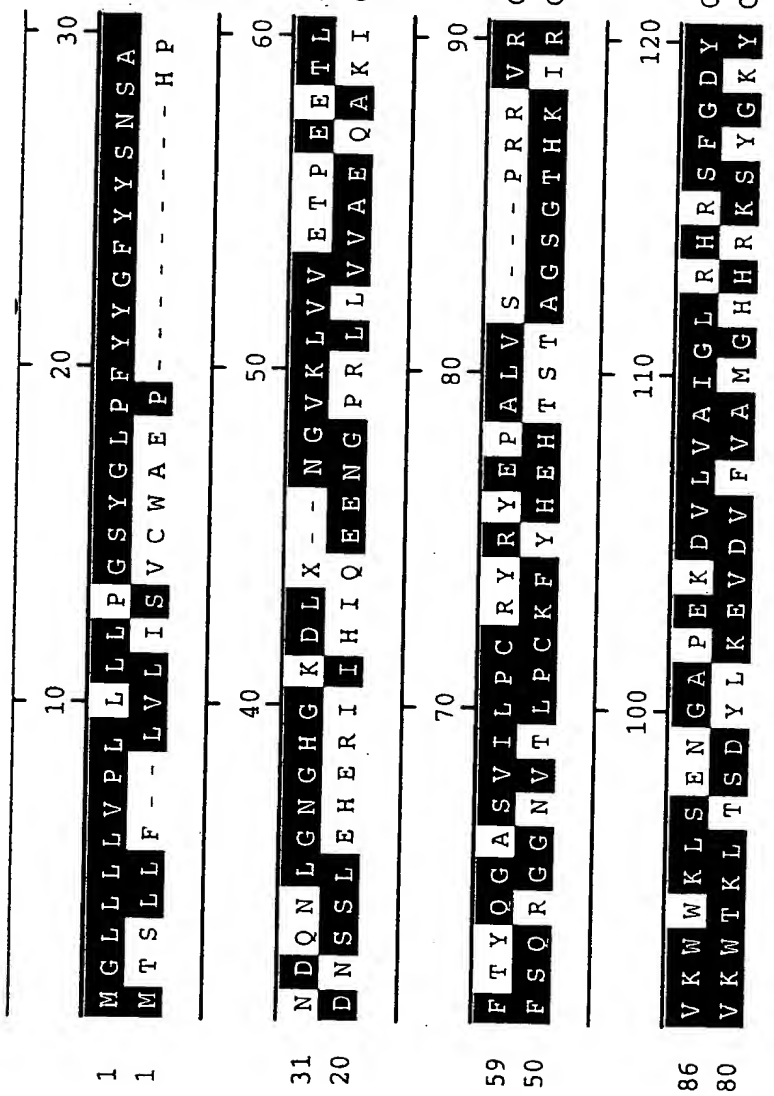

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FIGURE 7B

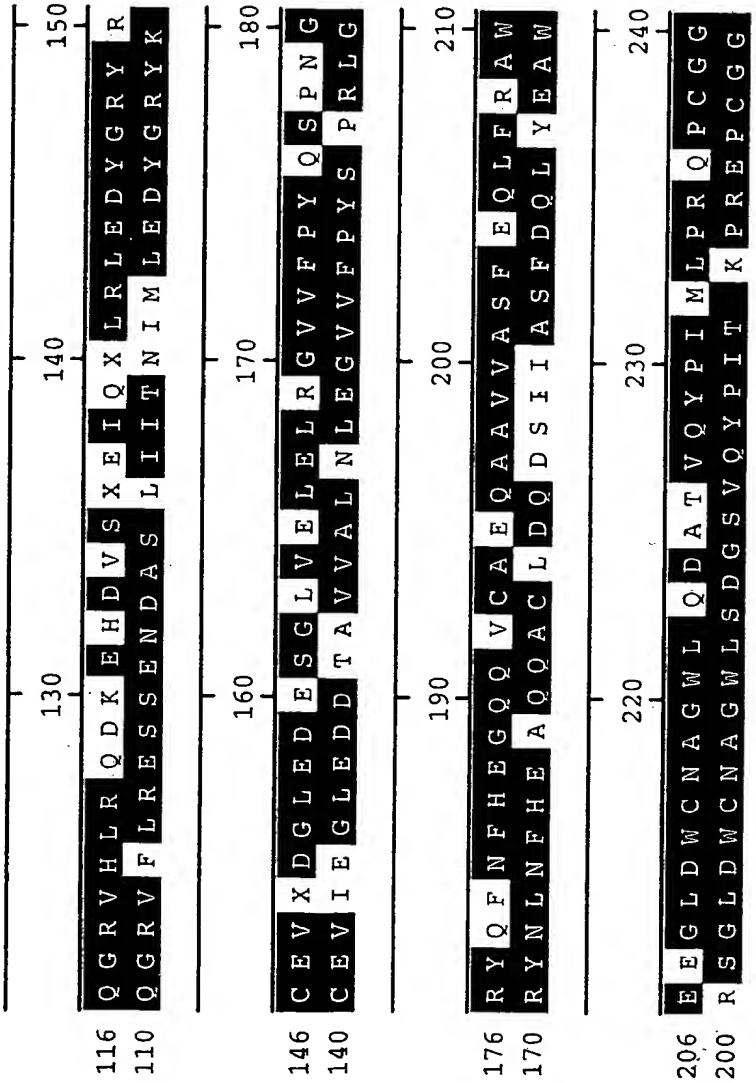

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FIGURE 7C

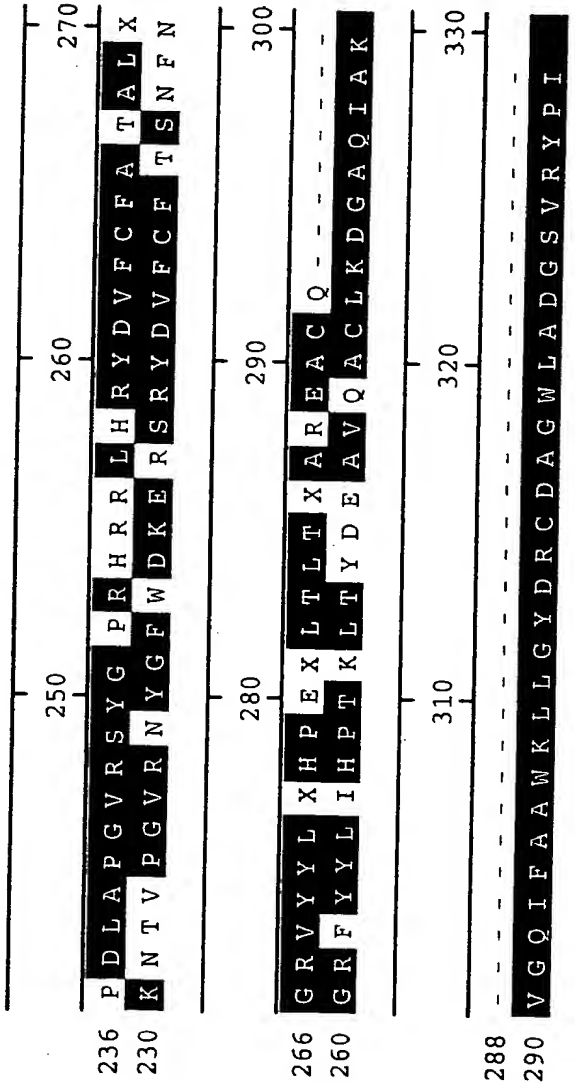

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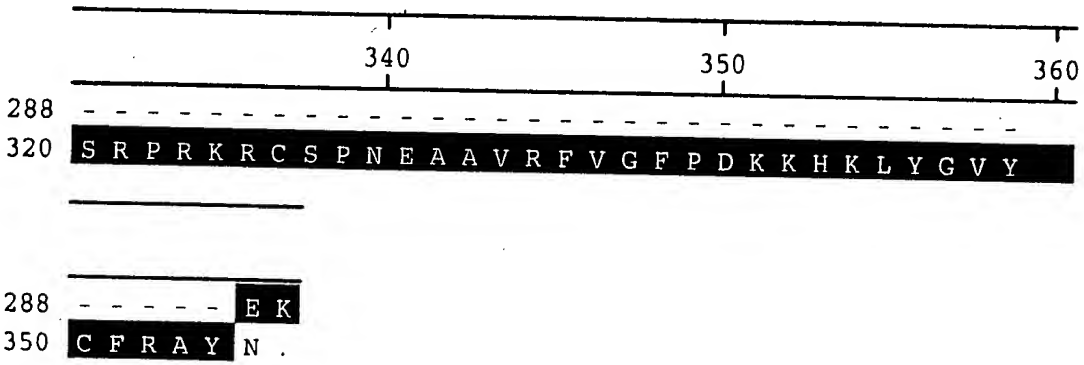
FIGURE 7D



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

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FIGURE 8A

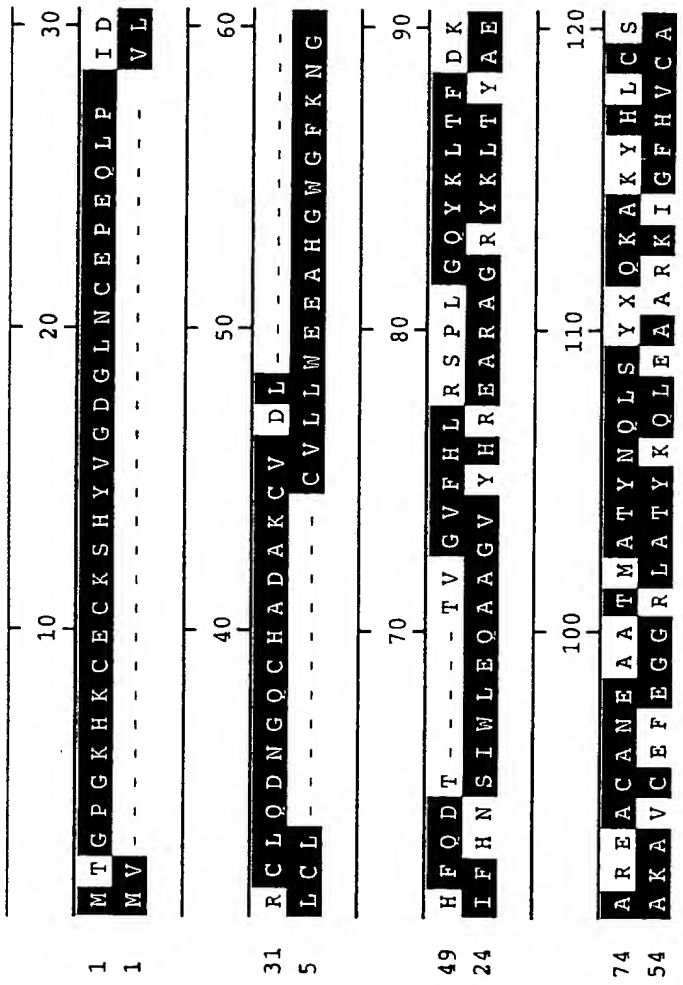

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FIGURE 8B

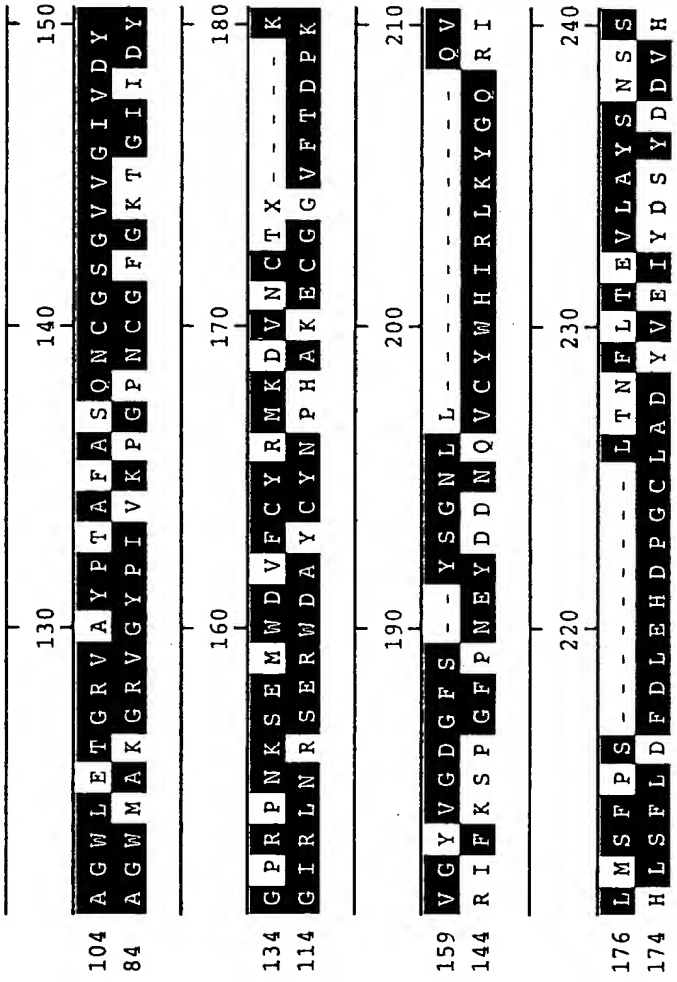

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FIGURE 8C

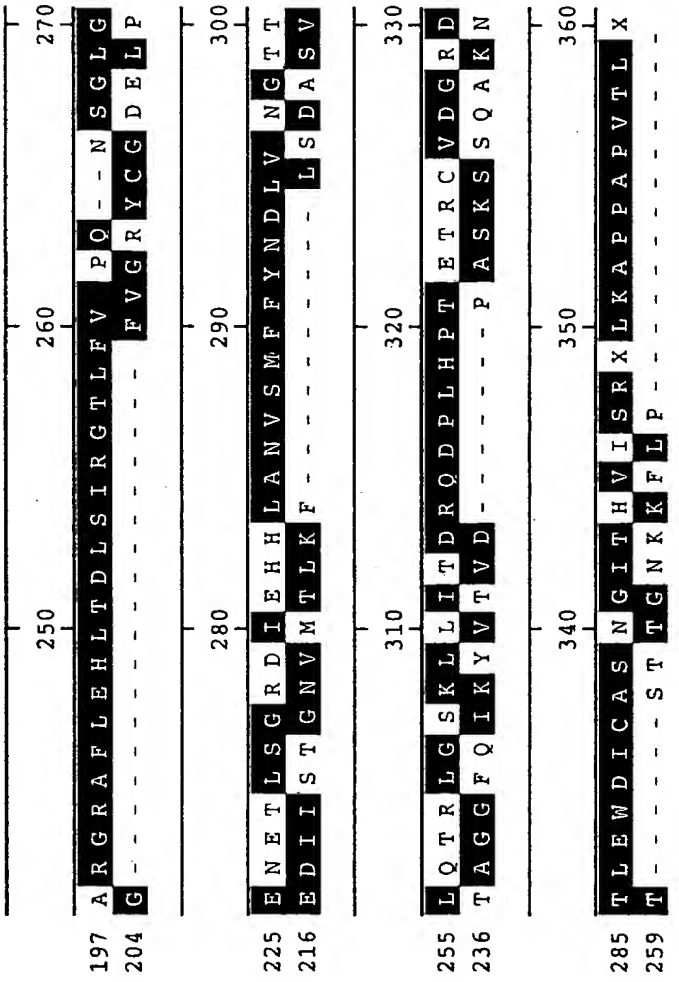

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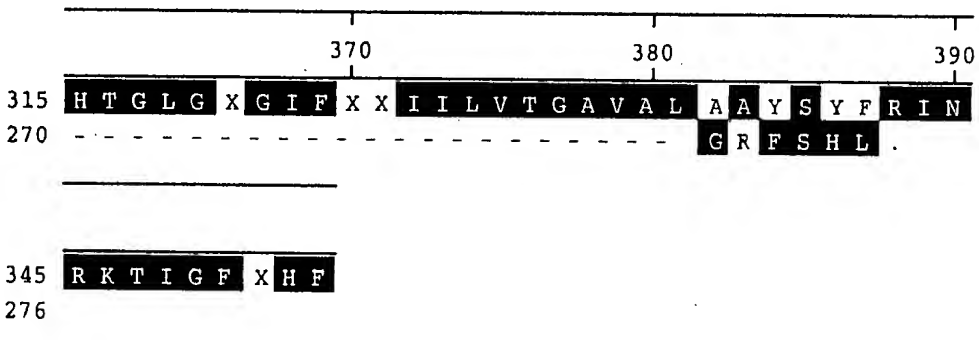
FIGURE 8D



BM-HABP AA SEQUENCE*
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BM-HABP AA SEQUENCE*
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Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

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FIGURE 9A

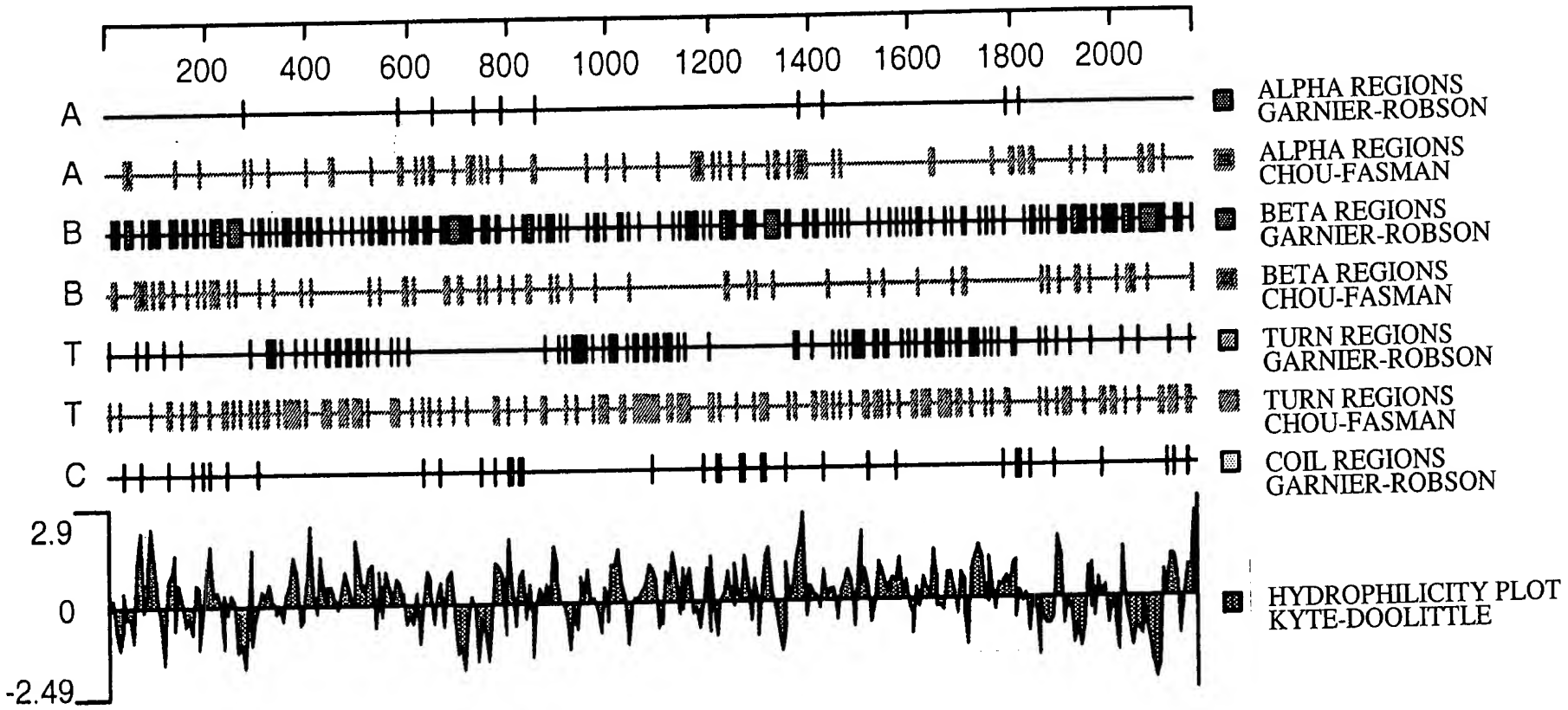

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FIGURE 9B

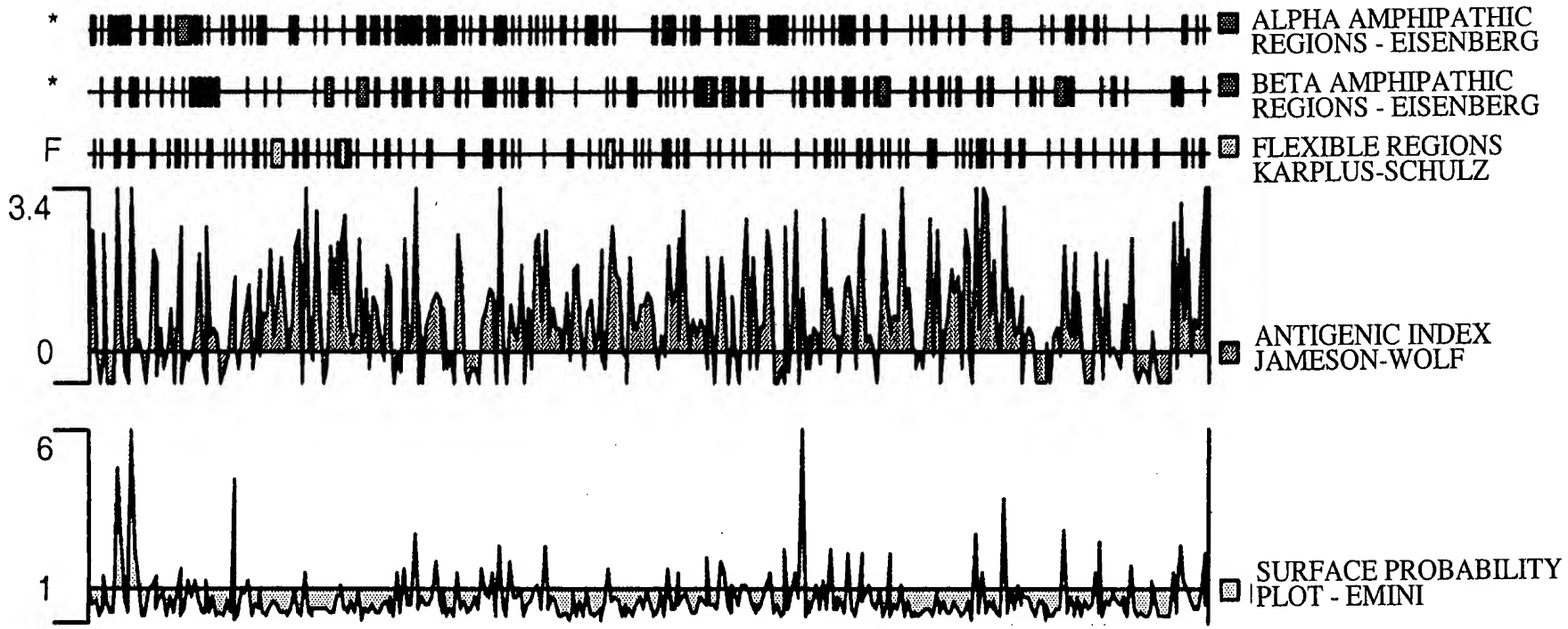

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FIGURE 10A

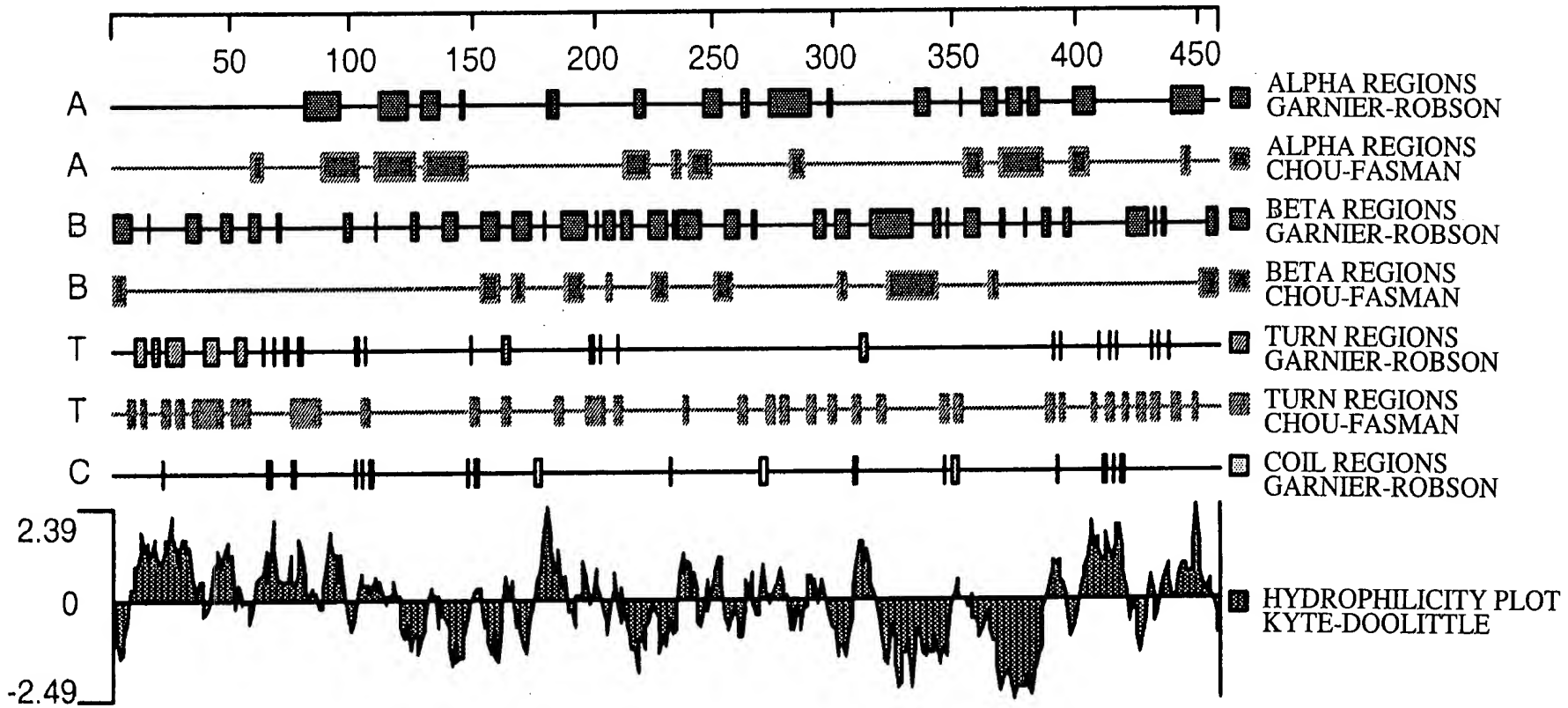

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FIGURE 10B

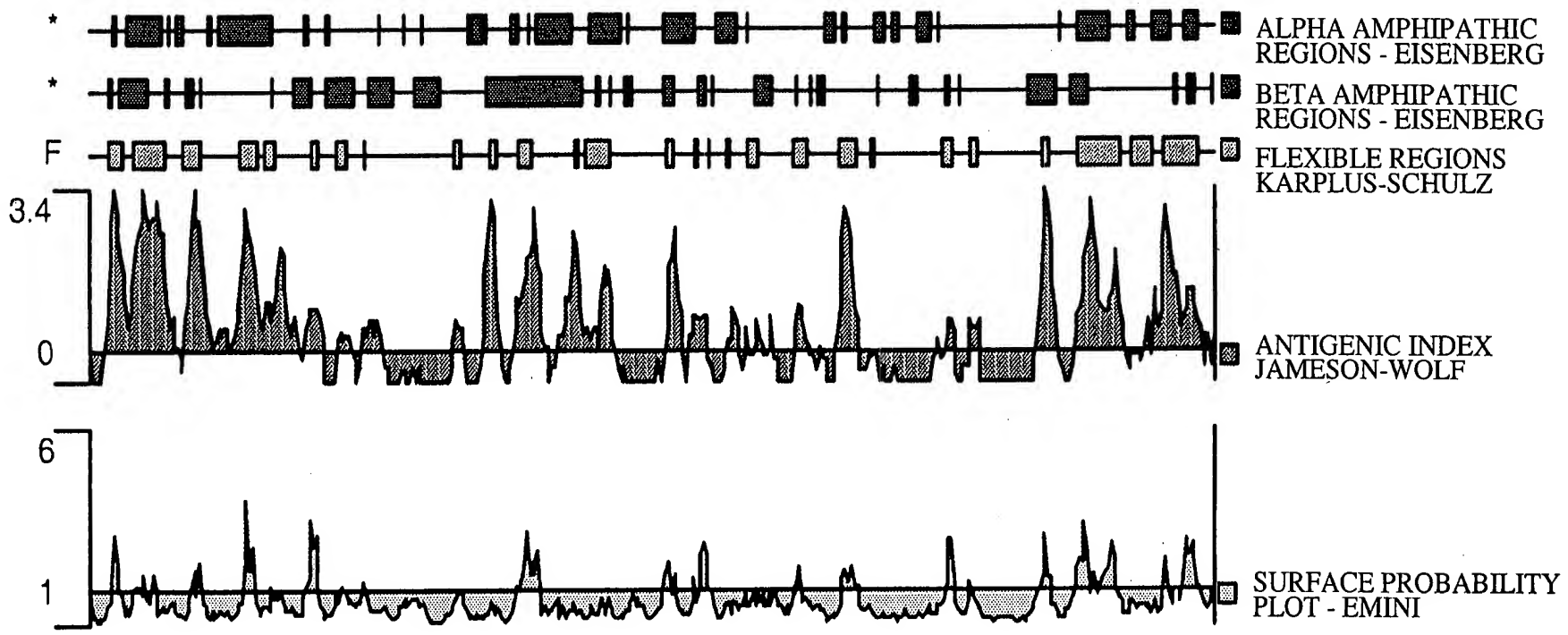

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FIGURE 11A

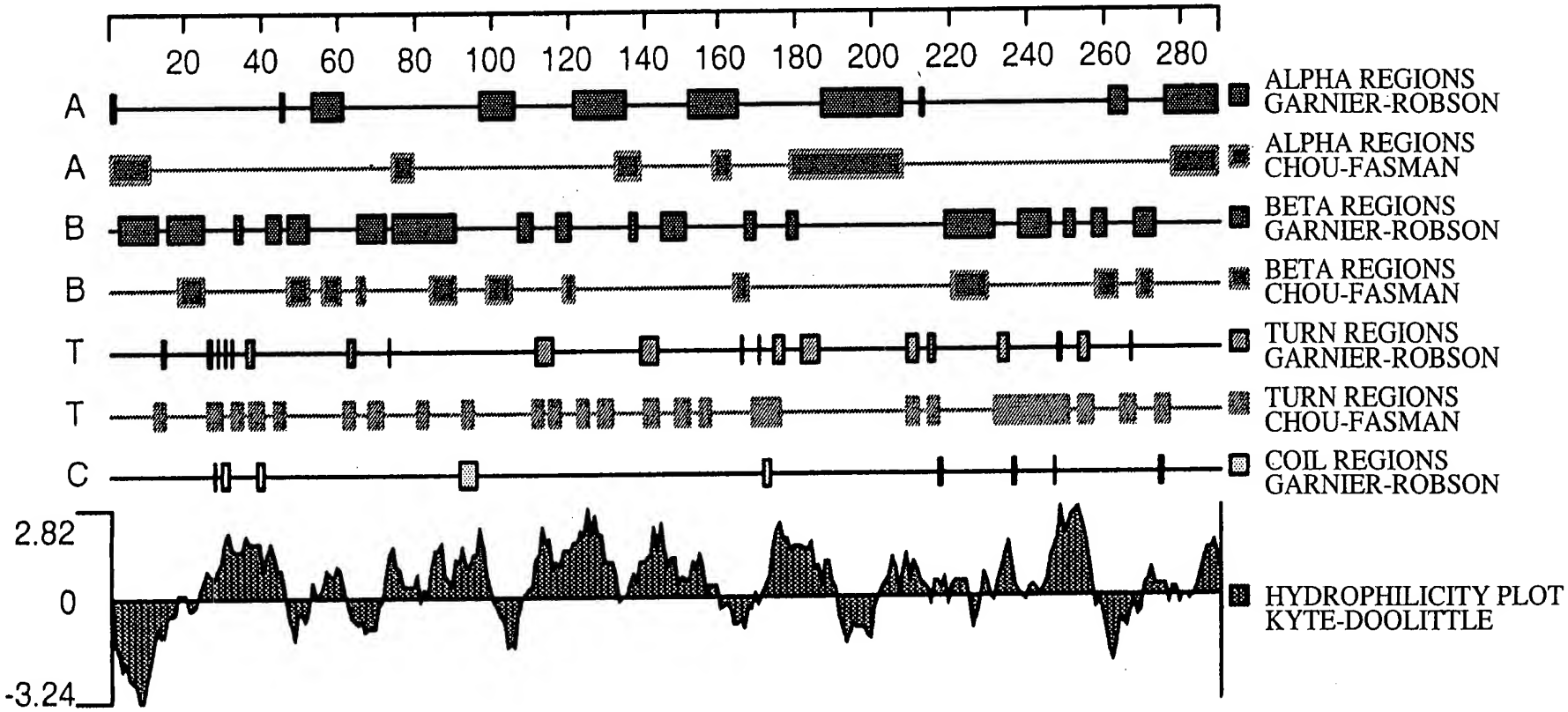

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FIGURE 11B

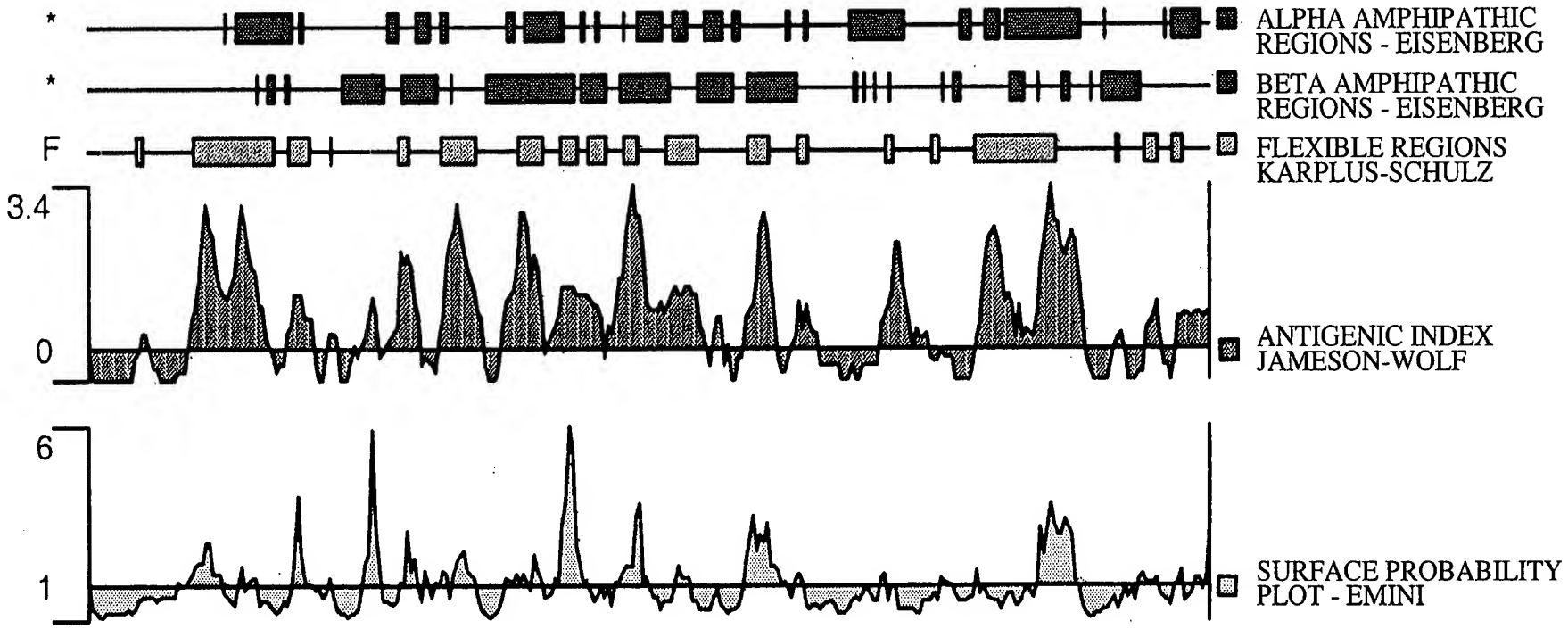

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FIGURE 12A

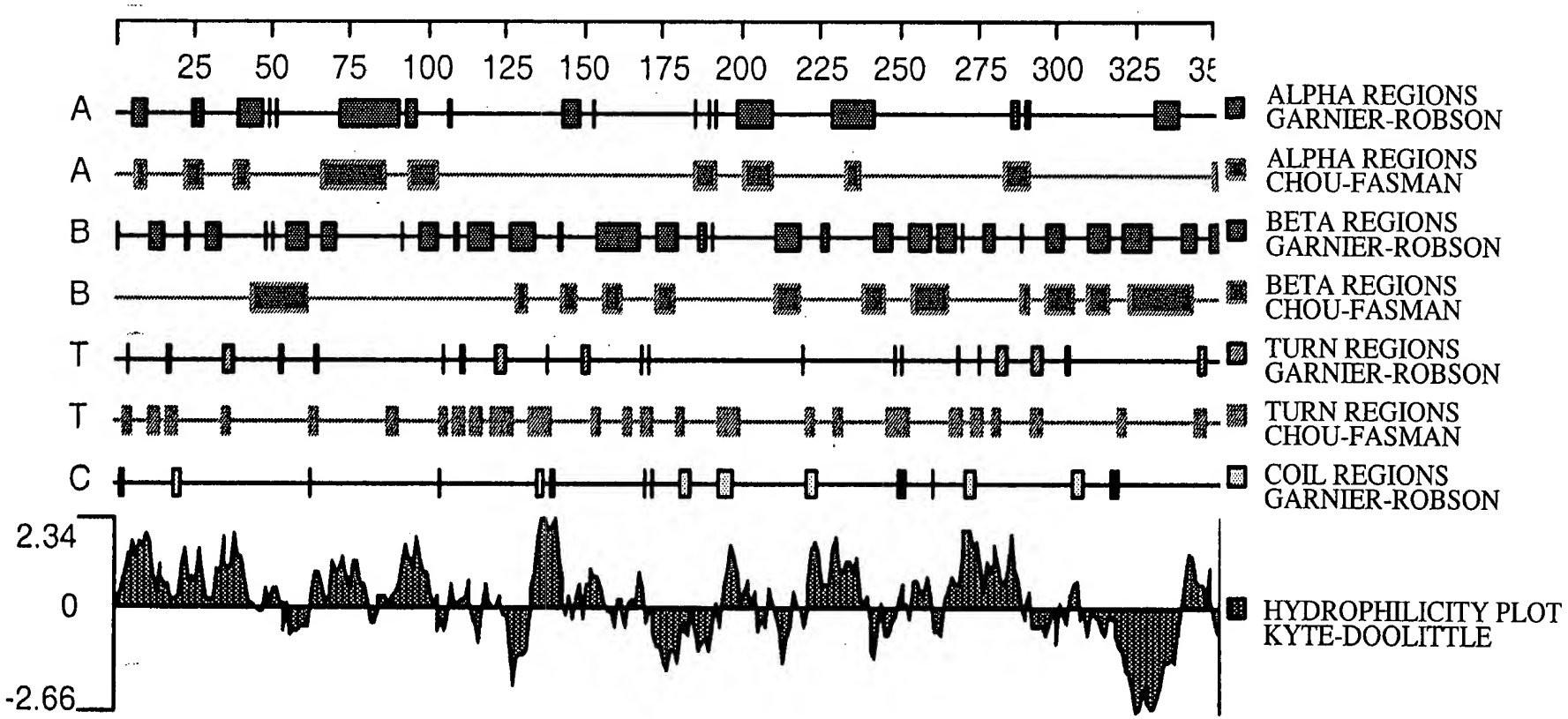

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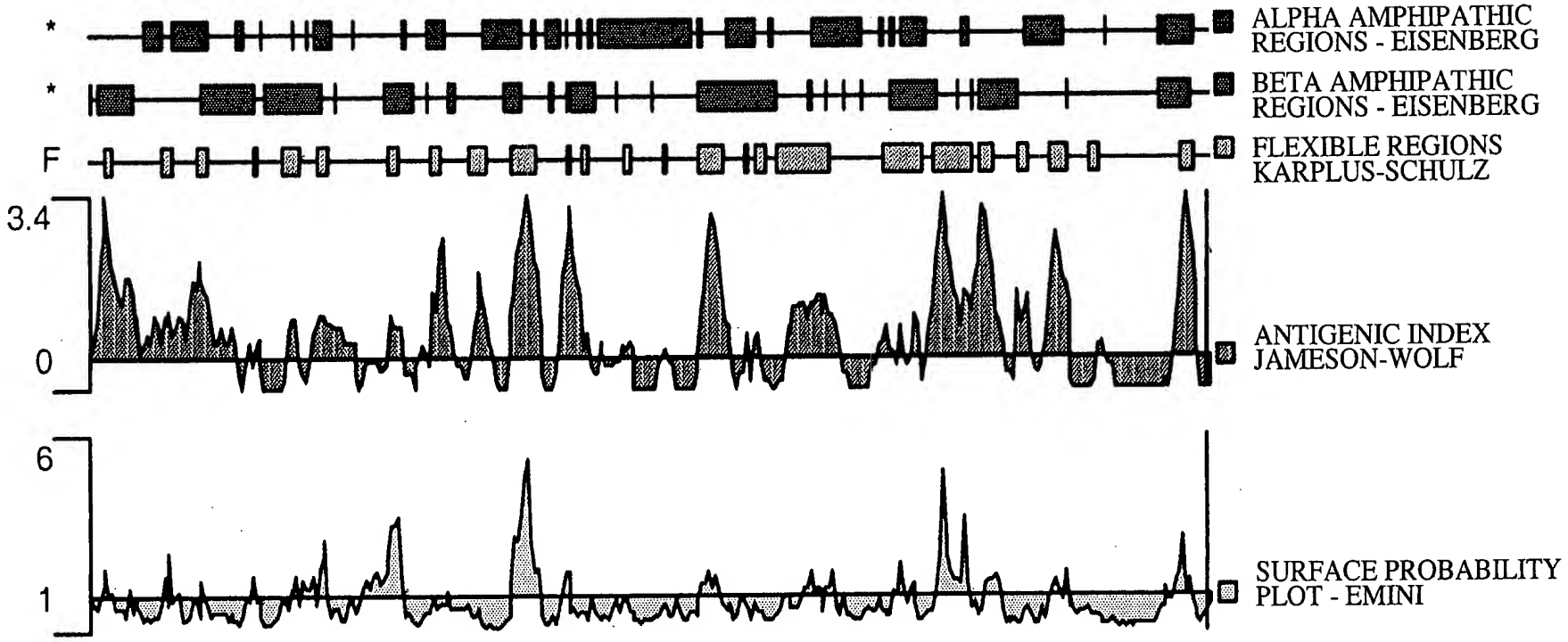
FIGURE 12B



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